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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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Title: Perfect score: Sequence: OM nucleic - nucleic search, using sw model Scoring table: Run on: IDENTITY\_NUC Gapext 1.0 US-09-905-674-1 1388 1 cttcctcggccgagccgggc.....gggaggcgngacgttggccc 1388 December 19, 2002, 02:23:32; Search time 2737 Seconds (without alignments) 14758.748 Million cell updates/sec

Total number of hits satisfying chosen parameters: 2054640 seqs, 14551402878 residues 4109280

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : gb\_ov:\*
gb\_pat:\*
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Pred. No. is the number of results predicted by chance to have em\_htgo\_hum:\*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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## ALIGNMENTS

TITLE JOURNAL	AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX440923	RESULT 1
Tetraspan protein and uses thereof Patent: WO 0206340-A 1 24-JAN-2002;	I Reinhard.C.T and Garcia p D	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	human.		AX440923.1 GI:21665563	AX440923		AX440923 1388 bp DNA linear PAT 28-,TIN-2002		

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                                                                                                                                                                                                                         Submitted (10-JUL-2002) GSF, Institut fuer Bioinformatik MIPS, Ingolstaedter Landstr. 1, 85764 Neuherberg, Germany Clone from S. Wiemann, Molecular Genome Analysis, German Cance Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center,
                                                                                                                                                                                                                                                                                                                                                                                                              complete cds. AL136638
                                                                                                                                                                                                 Heidelberg/Germany) within the cDNA sequencing German Genome Project.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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/clone="DKF2p564B1037"
/tissue_type="brain"
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/dev_stage="fetal"
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/chromosome="10"
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REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL KEYWORDS SOURCE ORGANISM FEATURES VERSION source Homo sapiens AF311903 AF311903.1 G Submitted (06-OCT-2000) Department of Immunology, Second Medical University & Shanghai Brilliance Biotechnology Ir 800 Xiangyin Rd., Shanghai 200433, P.R.China 1 (bases 1 to 2553) Zhang, W., Li, N., Wan, T. Identification of novel 2 (bases 1 to 2553) Zhang, W., Li, N., Wan, T. Unpublished
2 (hases 1 Eukaryota; Metazoa; Mammalia; Eutheria; Homo sapiens Direct Submission /organism="Homo:/db\_xref="taxon:973...885 /codon\_start=1 /product="DC-TM4F2 precursor" /protein\_id="AAM94899.1" ocation/Qualifiers GI:22266721 Chordata; Primates; and Cao, X. membrane proteins and Cao, sapiens" 1:9606" Craniata; Vertebrata; Catarrhini; Hominidae. Hominidae; Euteleostomi;

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                                      Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                    CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Cor DNA Sequencing by: National Institutes of F Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.
Contact: MGC help desk
Email: gagabs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                       Submitted (05-FEB-2001) National Institutes of Gene Collection (MGC), Cancer Genomics Office, Institute, 31 Center Drive, Room 11A03, Betheso
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 2502)
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distribution: gh the I.M.A.G
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MGC
Consortium/LLNL at:
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of Health Intramural
                information can
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National Cancer
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CCCCTTCTCCTGCTGCGTGCCAGATCCTGCGCAAAAAGTTGTGAACACACAGTGTGGATA 671
                                             CCTCATCGACTCCCTTCAGAAAGCTAACCAGTGCTGTGGCGCATATGGCCCTGAAGACTG
                                                                                                                                     CTTCCTGGAGCTGGCCGTGGCCGTGCTGCCTGTTCCAGGACTGGGTGAGGGACCG
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This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency analysis, Similarity but not identity to protein.

Location/Qualifiers
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/Product="Similar to transmembrane 4 superfamily member 9"
/Protein_id="AAH02920.1"
/db_xref="GI:12804133"
/translation="MHYYRYSMAKVSCMYKYLLESYNIIFWGYLSDLTKVTRNHGIDP
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RDRFREFFESNIKSYRDDIDLQNLIDSLQKANQCCGAKGPEDWDLNVVFNCSGASYSR
EKCGVPFSCCVPDPAGXVVNTQCGYDVRIQLKSKWDESIFTKGCIQALESWLFRNIYI
PAGVETANISLLQIEGIFTARTLISDIEAVKAGHHF"
3 625 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:11352 IMAGE:3954042"
/tissue_type="Skin, melanotic melanoma."
/clone_lib="NIH_MGC_20"
/lab_host="DH10B-R"
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95.3%;
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Pred. No. 4.9e-268;
2; Mismatches 8;
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Qy 672 Db 617	TGATGTCAGGATTCAGCTGAAGAGCAAGTGGGATGAGTCCATCTTCACGAAAGGCTGCAT 731
Оу 732	CCAGGCGCTGGAAAGCTGGCTCCCCGCGGAACATTTACATTGTGGCTGGC
Db 677	CAGGCGCTGGAAAGCTGGCTCCCGCGGAACATTTACATTGTGGCTGGC
ОУ 792	ATCTCGCTGTTGCAGATATTTGGCATCTTCC
Db 737	CATCTCGCTGTTGCAGATATTTGGCATCTTCCTGGCAAGGACGCTGATCTCAGACATCGA 796
Оу 852	GGCAGTGAAGGCCGGCCATCACTTCTGAGGAGCAGAGTTGAGGGAGCCGAGCTGAGCCAC 911
Db 797	GCAGTGAAGGCCGGCCATCACTTCTGAGGAGCAGAGTTGAGGGAGCCGAGCTGAGCCAC 856
Qу 912	GCTGGGAGGCCAGAGCCTTTCTCTCTGCCATCAGCCCTACGTCCAGAGGGAGAGGGAGG
Db 857	GCTGGGAGGCCAGAGCCTTTCTCTGCCATCAGCCCTACGTCCAGAGGGAGAGGAGCCGAC 916
Qy 972	ACCCCCAGAGCCAGTGCCCCATCTTAAGCATCAGCGTGACCTGTGCTCTGTTTTCTGCT 1031
Db 917	ACCCCCAGAGCCAGTGCCCCATCTTAAGCATCAGCGTGACGTGACCTCTCTGTTTCTGCT 976
103	TGCTGGTGCTGAAGACCAAGGGTCCCCCTTGTTACCTGCCCAAACTTGTGACCTGCATCCC 1091
Db 977	TGCTGGTGCTGAAGACCAAGGGTCCCCCTTGTTACCTGCCCAAACTTGTGACTGCATCCC 1036
Qy 1092	TCTGGAGTCTACCCAGAGACAGAGAATGTGTCTTTATGTGGGAGTGGTGACTCTGAAAGA 1151
Db 1037	TCTGGAGTCTACCCAGAGACAGAGAATGTGTCTTTATGTGGGAGTGGTGACTCTGAAAGA 1096
115	CAGAGAGGGCTCCTGTGGCTGCCAGGAGGGCTTGACTCAGACCCCCTGCAGCTCAAGCAT 1211
Ċ	CAGAGAGGCTUUTGTGCCTGCCAGGAGGGCTTGACTCAGACCCCCTGCAGCTCAAGCAT 1156
121	GTCTGCAGGACACCCTGGTCCCCCTCTCCAYTGGCWTCCAGACATCTGCTTTGGGTCATC 1271
Db 1157	GTCTGCAGGACACCCTGGT-CCCCTCTCCACTGGCATCCAGACATCTGCTTTGGGTCATC 1215
Qy 1272	CACATCTGTGGGTNGGCCGTGGGTAGAGGGACCCCACAGGCGTGGACAGGGCATCTCTCTC
Db 1216	ACATCTGTGGGTGGGCCGTGGGTAGAGGGGACCCACAGGCGTGGACAGGGCATCTCTCT
Qу 1332	CATCAAGCAAAGCAGGAGGGGCCTTGCCGTAAACGGGAGGCG 1376
Db 1276	ATCAAGCAAAGCAGCATGGGGG
RESULT 5 BC025568 LOCUS DEFINITION	BC025568 2428 bp mRNA linear ROD 07-AUG-200: Mus musculus, Similar to region containing hypothetical protein MC011353. Similar to region containing hypothetical protein
ACCESSION VERSION KEYWORDS	CGS: BC025568 BC025568.1 GI:19343883 MGC.
ORGANISM	nouse mouse. Mus musculus Eukaryota; Metazoa; Chordata: Craniata: Vertebrata: Futeleostomi
REFERENCE AUTHORS	lia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M sees 1 to 2428) berg R.
TITLE JOURNAL	Direct Submission Submisted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cqapbs-r@mail.nlh.gov

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FEATURES
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Best Local Similarity
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                                                                                                                                                         GCATGGAGCGAAAAGGGTGTGCTGTCCGACCTCACCAAAGTGACCCGGATGCATGGAATC
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TGCGTGGGGGCTCTGCGGGAGAATATCTGCTTGCTCAACTTTTTCTGTGGCACCATCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LIML at: http://image.lln Series: IRAK Plate: 56 Row: j Column: 21 This clone was selected for full length sequencing because passed the following selection criteria: GenomeScan generalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural
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protein McCl1352; slingshot"
/protein_id="AAH25568.1"
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/db_xref="GI:1934384"
/db_xref="GI:1934384"
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FILELAVAVLAFILFODWYBDRFREFFESNIKSYBDDIDLONLIDSLQKANQCCGAYGPE
DWDLNYFNCSGASYSREKCGVPFSCCVPDPAQKVVNTQCGYDVRIQLKSWDEFIFT
KGCIQALEGWLPRNIYIVAGVFTAISLLQIFGIFLARTLISDIEAVKAGHHF"
kGC13ALGGWLPRNIYIVAGVFTAISLLQIFGIFLARTLISDIEAVKAGHHF"

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/tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carchroma. 5 month old virgin mouse." /clone_lib="NCI_CGAP_Mam6" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: 64. .876
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/db_xref="taxon:10090"
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                                            Mus musculus, MGC11352; sli
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                                            slingshot,
            GI:19354053
                                           2498 bp mRNA linear ROD 07-AUG-2002
Similar to region containing hypothetical protein
ngshot, clone MGC:28503 IMAGE:4188261, mRNA, complete
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                                                            AACATCATCTTCTGGTTGGCTGGAGTTGTCTTCCTTGGAGTCGGGCTGTGGGCATGGAGC
                                                                                                                      TATTATAGATACTCGAACGCCGAGGTCAGCTGCTGCTACAAGTACCTGCTCTTCAGCTAC
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GAAAAGGGTGTGCTGTCCGACCTCACCAAAGTGACCCGGATGCATGGAATCGACCCTGTG
                                      AATATCGTCTTTTGGCTGGCTGGAGTTGTCTTCCTTGGAGTCGGGCTGTGGGCCATGGAGC
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium//LINI at: http://image.llnl.gov series: IRAK Plate: 37 Row: e Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.
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Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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DWDLNNYFNCSGASYSREKCGVPFSCCVPDDRACKVNNTQCGYDVRIQLKSKWDEFIFT
KGCIQALEGWLPRNIYIVAGVFIAISLLQIFGIFLARTLISDIEAVKAGHHF"
644 c 631 g 681 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Similar to region containing hypothetical protein MGC11352; slingshot"
/protein_id="AAH24611.1"
/db_xref="G1:19354054"
/translation="MHYYRYSNAEVSCWYKYLLFSYNIVFWLAGVVFLGVGLWAWSEK
/translation="MHYYRYSNAEVSCWYKYLLFSYNIVFWLAGVVFLGVGLWAWSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="MGC:28503 IMAGE:4188261"
/tissue_type="Salivary gland, 10
/clone_lib="NCI_CGAP_SG2"
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Eutheria;
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/db_xref="taxon:10090"
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Rodentia;
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TITLE
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                                                                      TAGATACTCTAACGCCAAAGTCAGCTGCTGGTACAAGTACCTCCTTTTCAGCTACAACAT 137
                                                                                                                                                          GGCCGCGCGCCGCCGCCGCCGCGCGCGCGTTCTCTCAGAAGATGCACTATTA
                                                                                                                                                                                                                         1009;
  CATCTTCTGGTTGGCTGGAGTTGTCTTCCTTGGAGTCGGGCTGTGGGCCATGGAGCGAAAA 197
                                            TAGATACTCGAACGCCGAGGTCAGCTGCTGCTACAAGTACCTGCTCTTCAGCTACAATAT
                                                                                                                                   GGCCGTGCTGCCGCCTGCCGCCCCCGGGTCCTCCTCTCAGAAGATGCACTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLML at: http://image.lln Series: IRAK Plate: 59 Row: a Column: 4
This clone was selected for full length sequencing because passed the following selection criteria: GenomeScan gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consorthum (LINL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, edu web site: http://www-shgc.stanford.edu Contect: (Dickson, Mark) mod@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 2500)
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                                                                                                                                                                                                                                                                                                                              /product="Unknown (protein for MGC:36554)"
/protein_id="AAH26574.1"
/protein_id="AAH26574.1"
/db_xref="GI:20072353"
/db_xref="GI:20072353"
/transilation="MHYYRYSNAEVSCWYKYLLFSYNIVFWLAGVVFLGVGLWAWSEK
GVLSDLTKVTRLHGIDPVVLVLMVGVVMFTLGFAGCVGALRENICLLKFFCGAIVLIF
FLELAVAVLAFLFQDWYNDRFREFFESNIKSYNDDIDLONLIDSLQKRNQCCGAYGPE
DWDLNYFNCSGASYSREKGGVPFSCCVPDPAQKVVNTQCGYDVRIQLKSKWDEFIFT
KGCIQALEGWLRRNIYLVAGVFIAISLLQIFGIFLARTLISDIEAVKAGHHF"
a 643 c 631 g 681 t
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/tissue_type="Mammary tumor. C3(1)-Tag model.
ductal carcinoma. 5 month old virgin mouse."
/clone_lib="WCI_CGAP_Mam6"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/db_xref="taxon:10090"
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Sciurognathi; Muridae;
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                                       GAGGCAGTGAAGGCCGCCCATCACTTCTGAGGAGCAGAGTTGAGGGAGCCGAGCTGAGCC
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Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-0c7-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oligo capping; fis (full insert sequence).
Homo sapiens fetus brain cDNA to mRNA, clone_lib:FEBRA2clone:FEBRA2000727.
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Isogai, T., Otsuki, T.
Direct Submission
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Mammalia; Eutheria;
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/db_xref="taxon:9606"
/clone="FEBRA2000727"
/tissue_type="brain"
/clone_lib="FEBRA2"
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                                                                                                                                                   Direct Submission
Submitted (3-APR-2002) Genome Therapeutics Corporation, 10
Street, Waltham, MA 02453, USA
On Apr 23, 2002 this sequence version replaced g1:18266617
Location/Qualifiers
                                                                                                                                                                                                                             Submitted (12-JAN-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA 3 (bases 1 to 161804)
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Homo sapiens chromosome 10 clone RP11-137H2, compl
ACO21028
                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                               Smith, D.R.
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 161804)
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                                                                                                                                                                                                                                                                                                                     Sequence Data
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                                                                                                                                       23228, a human tetraspanin family member patent: WO 0216603-A 3 28-FEB-2002; Millennium Pharmaceuticals, Inc. (US) Location/Qualifiers
                                                                                                                                                                                                         Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Hammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                          Score 362; DB Pred. No. 1.6e-0; Mismatches
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                                                                                                                          GCATCTGCCTGGCCCAGAACCTCGTGAGTGACATCAAGGCAGTGAAAGCC
                                                                                                                                                     GCATCTTCCTGGCAAGGACGCTGATCTCAGACATCGAGGCAGTGAAGGCC 864
                                                                                                                                                                                                                                                                 GCAAGTGGGATGAGTCCATCTTCACGAAAGGCTGCATCCAGGCGCTGGAAAGCTGGCTCC
                                                                                                                                                                                                                                                                                                                                                    GCACTGACTTGAACCCCAGCCGGGAGCGCTGCGGGGTGCCCTTCTCCTGCTGCGTCAGGG
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                                                                                                                                                                                AGGACAACCTGATTGTGGTGGCGGGAGTCTTCATGGGCATCGCCCCTCCTCCAGATCTTTG
                                                                                                                                                                                                                                        TGGAGCAGCAGGCTTCATCCACACCAAAGGCTGCGTGGGCCAGTTTGAGAAGTGGCTGC
                                                                                                                                                                                                                                                                                              ACCCTGCGGAGGATGTCCTCAACACCCAGTGTGGCTACGACGTCCGGCTCAAACTGGAGC
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BC010346
Mus musculus, RI
IMAGE:2811935, n
BC010346
BC010346.1 GI:
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                                        linear ROD clone MGC:6941
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TGGGCGTGGTGATGTTCACCCTGGGGTTCGCCGGCTGCGGGGGCTCTGCGGGAGAAATA 328
                                                                                                                                                                                            TGGCTGGAGTTGTCTTCCTTGGAGTCGGGCTGTGGGCATGGAGCGAAAAGGGTGTGCTGT 208
                                                                                                                                                                                                                                                                                            ACGCCAAAGTCAGCTGCTACAAGTACCTCCTTTTCAGCTACAACATCATCTTCTGGT 148
                                                                           CCAACATCTCGGCGGCTGACAGATCTGGGCGGCTCTTGACCCCCGTGTGGCTGTTTGTGGTGG
                                                                                                  CCGACCTCACCAAAGTGACCCGGATGCATGGAATCGACCCTGTGGTGCTGGTCCTGATGG
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509; Conserv
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Direct Submission
Submitted (05-JUL-2001) National Institutes of Headene Collection (MGC), Cancer Genomics Office, National Institute, 31 Center Drive, Room 11A03, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAK Plate: 5 Row: f Column: 18.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Hump
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, Yoon, V.S., Kowis, C.R., Lawrence, S., Martin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGC.
house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="LocusID:74257"
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PNDWHLMIYFMCTDLAPSRERGGVPFSCCVRDPAEDVLNTQCGYDIRLKLELEQQGSI
YTKGCVGQFEKWLQDMLIVYAAGVVLGALLQIFGLCLAQNLVSDIKAVKANW"
461 g 361 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="RIKEN cDNA 2210021G21
/protein_id="AAH10346.1"
/db_xref="GI:16307593"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B"
/note="Vector"
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old. gross tissue."
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/db_xref="taxon:10090"
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65.6%;
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Pred. No. 1.7e-69;
0; Mismatches 267
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                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
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                                                                                           cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: ammadan@systemsbiology.org Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephar
                                                                                                                                                                                                                                                                                                   Submitted (09-JUL-2001) National Institutes of Gene Collection (MGC), Cancer Genomics Office, Institute, 31 Center Drive, Room 11A03, Betheso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens,
MGC:14859 IMAG
Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAL Plate: 24 Row: k Column: 15
                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.
Contact: MGC help desk
Email: cgqbbs:r@mail.nih.gov
Tissue Procurement: ATCC
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1 (bases 1 to 2426)
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IMAGE:3621871, mRNA, of
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cDNA 2210021G21 gene,
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                       http://image.llnl.gov
                                        information can be
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National Cancer
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                                                                                                                                                ACTGGTCTTGCTGCGGAGCCCCGAGGCCCCCAATGACTTGGAACCTCAATATCTACTTCAACT
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CGCGGAACATTTACATTGTGGCTGGCGTCTTCATCGCCATCTCGCTGTTGCAGATATTTG
                                                        GCAAGTGGGATGAGTCCATCTTCACGAAAGGCTGCATCCAGGCGCTGGAAAGCTGGCTCC
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//db_xref="GI:14714541"
//db_xref="GI:14714541"
//db_xref="GI:14714541"
//translation="morekiOHFOEPEVGCCGKYFLFGFNIVFWYLGALFLAIGLWAWG
/translation="morekiOHFOEPEVGCYMSVLGFAGCIGALRENTFLLKFFSVFLGL
EKGYLSNISALTDLGGLDPVWLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGL
EFFLELATGILAFVFKDWIRDOLNLFINNNVRAYRDDIDLQNLLDFAGEYWSCCGARG
PNDWNLNIYFNCTDLNPSRERCGVPFSCCVRDPAEDVLNTQCGYDVRLKLELEQQGFI
PNDWNLNIYFNCTDLNPSRERCGVPFSCCVRDPAEDVLNTQCGYDVRLKLELEQQGFI
HTKGCVGOFEKKILQDNLLVVAGVFWGIALLQIFGICLAQNLEQME"
a 662 c 716 g 541 t
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/tissue_type="Pancreas, adenocaro
/clone_lib="NIH_MGC_39"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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            TGTGGGCATGGAGCGAAAAGGGTGTGCTGTCCGACCTCACCAAAGTGACCCGGATGCATG
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GAATCGACCCTGTGGTGCTGGTCCTGATGGTGGGCGTGATGTTCACCCTGGGGTTCG
                                                                                           TGTGGGCGTGGAATGAAAAAGGTGTCCTCCCAACATCTCGTCCATCACCGACCTCGGTG
                                                                                                                                           TCATTTTTGGCTTCAATGTCATATTTTGGTTTTTTGGGAATAACGTTTCTTGGAATCGGAC
                                                                                                                                                                                          CCCAGAGGATGTCCGGGAAGCACTACAAGGGTCCTGAAGTCAGTTGTTGCATCAAATACT
                                                                                                                                                                                                                                         al Similarity
516; Conser
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Submitted (20-JAN-1999) Dept.
University of Barcelona, Av.
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Garcia-Frigola, C., d
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llarity 63.8%;
Conservative
                                                                                                                                                                                                                                                                                                /product="tetraspanin Tspan-5"
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KGCVPQFFKWLDNLTIVAGIFIGIALLQIFGICLAQNLVSDIEAVRASW"
a 811 c 840 g 857 t
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388. .1194
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Swiss Webster/NIH"
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Submitted (14-MAY-1998) INSERM U268,
Villejuif 94807, France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1405)
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/product="tetraspan NET-4"
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/translation="MSCKHYKGPEVSCCIKYFILGFAGCIGALRENTFLLKFFSVFLGIIF
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BASE COUNT ORIGIN Ω 멍 QΥ В Š 당 Ωy В В 9 В δÃ B δÃ 뮹 δÃ В δ B δ 밁 γ 뫄 Ş В Q Š 밁 Query Match Best Local Similarity Matches 524; Conservat 1094 1034 494 213 434 374 TGAAGTCAGTTGTTGCATCAAATACTTCATATTTTGGCTTCAATGTCATATTTTGGTTTTT 314 GCTGCCGGGGCAAGTGTCTTCATGAACCCAGAGGATGTCCGGGAAGCACTACAAGGGTCC 554 273 153 513 734 453 674 393 614 333 693 914 633 854 573 794 93 CAAAGTCAGCTGCTGGTACAAGTACCTCCTTTTCAGCTACAACATCATCTTCTGGTTGGC 152 33 GCCGCCGCGCGCGCGGATTCTGCTTCTCAGAAGATGCACTATTATAGATACTCTAACGC CGTGCTGGCCTTCCTGTTCCAGGACTGGGTGAGGGACCGGTTCCGGGAGTTCTTCGAGAG 452 CAACATCAAGTCCTACCGGGACGATATCGATCTGCAAAACCTCATCGACTCCCTTCAGAA 512 AGGAGTGATGTTCATTTTGGGATTTGCAGGGTGCATTGGAGCGCTACGGGAAAACACTTT CATCTCTTCCATCACCGATCTCGGCGGCTTTGACCCAGTTTGGCTCTTTCCTTGTGGTGGG CCTCACCAAAGTGACCCGGATGCATGGAATCGACCCTGTGGTGCTGGTGCTGATGGTGGG CCTTCTCAAGTTTTTTTCTGTGTTCCTGGGAATTATTTTCTTCCTGGAGCTCACTGCCGG CTTGCTCAACTTTTTCTGTGGCACCATCGTGCTCATCTTCCTTGCAGCCTGGCCTGTGGC 392 CGTGGTGATGTTCACCCTGGGGTTCGCCGGCTGCGTGGGGGGCTCTGCGGGAGAATATCTG 332 TTGCACAGATTCCAATGCAAGTCGAGAGCGATGTGGCGTTCCATTCTCCTGCTGCACTAA 913 CCCGCGGAACATTTACATTGTGGCTGGCGTGTTCATCGCCATCTCGCTGTTGCAGATATT 812 GAGCAAGTGGGATGAGTCCATCTTCACGAAAGGCTGCATCCAGGCGCTGGAAAGCTGGCT 752 TTGCAGCGGTGCCAGCTACAGCCGAGAGAAGTGCGGGGTCCCCTTCTCCTGCTGCGTGCC TGGGATATGCCTGGCCCAGAATTTGGTTAGCGATATCGAAGCTGTCAGGGCGAGC 1148 TGGCATCTTCCTGGCAAGGACGCTGATCTCAGACATCGAGGCAGTGAAGGCCGGC 867 AGTTGACCAGCAGATTGTAATCTACACGAAAGGCTGTGTGCCCCAGTTTGAGAAGTGGTT 309 Conservative D FLELTAGVLAFVFKDWIKDQLYFFINNNIRAYRDDIDLQNLIDFTQEYWQCCGAFGAD DWNLNIYFNCTDSNASRERCGVPFSCCTKDPAEDVINTQCGYDARQKPEVDQQIVIYT KGCVPQFEKWLQDNLTIVAGIFIGIALLQIFGICLAQNLVSDIEAVRASW" a 357 c 387 g 352 t 24.3%; 0; Score 337.4; DB 9; Length 1405; Pred. No. 7.1e-67; 0; Mismatches 311; Indels 0; Gaps 433 92 373 1033 613 553 272 1093 632 673 0;

Search completed: December Job time: 2928 secs 19, 2002, 04:48:40

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US-09-123-912-14
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#### ALIGNMENTS

US/09188930A

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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrist, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cel
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 62
LENGTH: 399
; Sequence 243, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
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Best Local Similarity
Matches 117; Conserv
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ORGANISM: mouse
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Pred. No. 2
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2.8e-12;
nes 62;
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; ORGANISM: Mouse
US-09-188-930-243
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 243
LENGTH: 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2. Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 117; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: IKEYAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Compositions Isolated From Skin Cells TITLE OF INVENTION: and Methods For Their Use
                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865552
FILING DATE: 09-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MONOCLONAL ANTIBODY, TITLE OF INVENTION: PRODUCTION THEREOF
                                                                                                                                                                      PRIOR APPLICATION DATA:
PRIOR APPLICATION NIMBER: JP 079996-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                    PRIOR APPLICATION DATA:
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                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                            PRIOR APPLICATION DATA:
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CITY: I
STATE:
                                                                                                        APPLICATION NUMBER: JP 0:
FILING DATE: 17-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 02109
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                                                      APPLICATION NUMBER: JP 022321-1992 FILING DATE: 07-FEB-1992
                                                                                                                                                               APPLICATION NUMBER: JP 07 FILING DATE: 12-APR-1991
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5439886
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                    RESNICK,
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MIYAKE, MASAYUKI
SENOO, MASAHARU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 WATER STREET
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NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
DAVID S.
MBER: 34235
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                                                                                                                           JP 085396-1991
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Pred. No. 2.8e
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2.8e-12;
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                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                         Sequence 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Keyama, Masaru
APPLICANT: Koyama, Masaru
APPLICANT: Miyake, Masanyki
APPLICANT: Senoo, Masaharu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
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                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE:
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                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 AGTCAGCTGCTGGTACAAGTACCTCCTTTTCAGCTACAACATCATCTTCTGGTTGGCTGG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL TYPE:
                                COUNTRY: UP
ZIP: 02109
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                                                                STATE:
                                                                             CITY: Boston
                                                                                                STREET:
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                                                                                                                                                                                                                                                                                                                                                                                            CGAGAGCAACATCAA 461
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99; Conservative
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                                                                                                  130 Water Street
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53.1%;
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Pred. No. 1
                                                                                                                 Roberts & Cushman
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CURRENT APPLICATION DATA:

FastSEQ Version 1.5 IBM Compatible

OPERATING SYSTEM:

FILING DATE:

22-MAR-1995

US/08/408,222B

CLASSIFICATION: APPLICATION NUMBER:

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 41777-DIV
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/254,493
FILING DATE: 06-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: JP-085396-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL: I
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                447
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375
                                                                                                                                     255 CCAGTGCATGCTGGGACTGTTCTTCGGCTTCCTCGTGATATTCGCCATTGAAATAGC
                                                                                                                                                                      327 TATCTGCTTGCTCAACTTTTTCTGTGGCACCATCGTGCTCATCTTCTTCCTGGAGCTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP-022321-1992 FILING DATE: 07-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
CAAGGACACCTACAA 389
                                                                   TGCGGCCATCTGGGGATATTCCCCACAAGGATGAGGTGATTAAGGAAGTCCAGGAGTTTTA 374
                                                                                                                                                                                                            AGCCGGCGCCCTCATGATGCTGGTGGGCTTCCTGGGCTGCTGCGGGGCTGTGCAGGAGTC
                                                                                                                                                                                                                                            GGTGGGCGTGGTGATGTTCACCCTGGGGTTCGCCGGCTGCGTGGGGGCTCTGCGGGAGAA 326
                                                                                                                                                                                                                                                                            CGAGCAAGAAACTAATAATAATTCCAGCTTCTACACAGGAGTCTATATTCTGATCGG
                             CGAGAGCAACATCAA 461
                                                                                                    TGTGGCCGTGCTGGCCTTCCTGTTCCAGGACTGGGTGAGGGACCGGTTCCGGGAGTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199;
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617-523-6440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA to genomic RNA
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53.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 69.8; DB 1;
Pred. No. 1.8e-09;
0; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 687;
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96 AGTCAGCTGCTGGTACAAGTACCTCCTTTTCAGCTACAACATCATCTTCTGGTTGGCTGG 155

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US-08-408-222B-3
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Best Local Similarity Matches 199; Conserv
                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-0
FILING DATE: 07-FEB-1994
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-0
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                            HYPOTHETICAL: 1
                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 22-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                    CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/254,493
                                                                         OTHER INFORMATION:
                                                                                          LOCATION:
                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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                                                                                                                                                                                                                                                                                                    1120 base pairs
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                                                                                          Coding Sequence 112...795
                                                                                                                                    breast carcinoma ZR-75-1
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                                                                                                                                                                                                                                                                      double
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                 53.1%;
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   0;
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 Score 69.8; DB 1;
Pred. No. 2.2e-09;
0; Mismatches 167;
                               Length 1120;
    Indels
    9;
   Gaps
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FILE REFERENCE: SUNY
CURRENT APPLICATION NUMBER: US/09/333,599
CURRENT FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 827
TYPE: DNA
ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: (57)..(815)
US-09-333-599-5
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US-09-333-599-5
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09333599 Patent No. 6245898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Quigley, James P.
APPLICANT: Seandel, Marco
TITLE OF INVENTION: MONOCLONAL ANTIBOIDES THAT RECOGNIZE ANTIGENS
TITLE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Testa, Jacqueline E.
    334
                                                                                                                  217 A---CCAAAGTGACCCGGATGCATGGAATCGACCCTGTGGTGCTGGTCCTGATGGTGGGC
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GTGGTGATGTTCACCCTGGGGTTCGCCGGCTGCGTGGGGGGCTCTGCGGGAGAATATCTGC
                                                                                                                                                                                                                               GTCAGCTGCTGGTACAAGTACCTCCTTTTCAGCTACAACATCATCTTCTGGTTGGCTGGA 156
                                                                                       CTGGCCTCAGGCACCTACCTGGCCACAGCCTACATCCTGGTGGTGGCGGGCACTGTCGTC
                                                                                                                                                                    GTTGTCTTCCTTGGAGTCGGGCTGTGGGCATGGAGCGAAAAGGGGTGTGCTGTCCGACCTC 216
                                                                                                                                                                                                            TGTGGCCGTGCTGCCTGTTCCAGGACTGGGTGAGGGACCGGTTCCGGGAGTTCTT
                              ATGGTGACTGGGGTCTTGGGCTGCTGCGCCACCTTCAAGGAGCGTCGGAACCTGCTGCGC
                                                                                                                                                   CTGGCTGTCATGGCAGTGGGCATCTGGACGCTGGCCCTCAAGAGTGACTACATCAGCCTG
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ilarity 48.4%;
Conservative
                                                                                                                                                                                                                                                                        Score 68.6; DB 4;
Pred. No. 4e-09;
0; Mismatches 234;
                                                                                                                                                                                                                                                                          234;
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; LENGTH: 870
; TYPE: DNA
; ORGANISM: Homo s
US-09-333-599-1
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APPLICANT: Quigley, James P.
APPLICANT: Seandel, Marco
TITLE OF INVENTION: MONOCLONAL ANTIBOIDES TO
TITLE OF INVENTION: ASSOCIATED WITH TUMOR MI
FILE REFERENCE: SUNY
CURRENT APPLICATION NUMBER: US/09/333,599
CURRENT FILLM DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
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LENGTH: 870
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Best Local Similarity
Matches 222; Conserv
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                                                                                                                                                            GTGCTGGCCTTCCTGTTCCAGGACTGGGTGAGGGACCCGGTTCCGGGAGTTCTTCGAGAGC
GAGTTCCACTGCTGGCCAGCAACAACTCACAGGACTGG
                        GCTAACCAGTGCTGTGGCGCATATGGCCCTGAAGACTGG 552
                                                                                                                                TACGCCTACTACCAGCAGCTGAACACGGAGCTCAAGGAGAACCTGAAGGACACCATGACC
                                                                AAGCGCTACCACCAGCCGGGCCATGAGGCTGTGACCAGCGCTGTGGACCAGCTGCAGCAG
                                                                                              AACATCAAGTCCTACCGGGACGATATCGATCTGCAAAACCTCATCGACTCCCTTCAGAAA 513
                                                                                                                                                                                                CTGTACTTCATCCTGCTCCTCATCATCTTTCTGCTGGAGATCATCGCTGGTATCCTCGCC
                                                                                                                                                                                                                                                                   ATGGTGACTGGGGTCTTGGGCTGCTGCGCCACCTTCAAGGAGCGTCGGAACCTGCTGCGC
                                                                                                                                                                                                                                                                                                                                  CTGGCCTCAGGCACCTACCTGGCCACAGCCTACATCCTGGTGGTGGCGGCACTGTCGTC
                                                                                                                                                                                                                                                                                                                                                       A---CCAAAGTGACCCGGATGCATGGATGGACCCTGTGGTGCTGGTCCTGATGGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                             GTTGTCTTCCTTGGAGTCGGGCTGTGGGCATGGAGCGAAAAAGGGTGTGCTGTCCGACCTC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGTTCCACTGCTGTGGCAGCAACAACTCACAGGACTGG 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTAACCAGTGCTGTGGCGCATATGGCCCTGAAGACTGG 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTIBOIDES WITH TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                               453
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US-08-254-493-3
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-5400
TELEFAX: (617) 523-6440
TELEEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 196; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865552
FILING DATE: 09-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: MONOCLONAL TITLE OF INVENTION: PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 00 FILING DATE: 17-APR-1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 00 APPLICATION NUMBER: J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DRIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                    CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: RESNICK, DAVID S. REGISTRATION NUMBER: 34235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 12-AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                         NAME/KEY:
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MIYAKE, MASAYUKI
      Conservative
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112..795
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115..795
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ZR-75-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP 022321-1992
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          0;
   Score 65; DB 1; Length 1120; Pred. No. 4.3e-08; O; Mismatches 170; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-08-705-771-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08705771 Patent No. 6054289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Paul M
APPLICANT: Jian N
                                                                                                                                                                                                              SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08
FILING DATE: August 30, 19
CLASSIFICATION: 536
ATTORNEY_AGENT INFORMATION:
NAME: MULLINS, J.G.
                                                                                                         TELEFAX: 973-994-1744
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
TOPOLOGY: 1
MOLECULE TYPE:
                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 AGGCACCAAGTGCATCAAATACCTGCTGTTCGGATTTAACTTCATCTTCTGGCTTGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     447 CGAGAGCAACATCAA 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366 CCAGTGCATGCTGGGACTGTTCTTCGGCTTCCTCTTGGTGATATTCGCCATTGAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 AGTCAGCTGCTGGTACAAGTACCTCCTTTTCAGCTACAACATCATCTTCTGGTTGGCTGG
                                                      TYPE:
                                                                                                                                                                           REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY:
                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: CARELLA, BYRNE, BAIN, GIL
ADDRESSEE: CECCHI, STEWART & OLSTEIN
                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTGGCCGTGCTGGCCTTCCTGTTCCAGGACTGGGTGAGGGACCGGTTCCGGGAGTTCTT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATCTGCTTGACTTTTTTTTTGTGGCACCATCGTGCTCATCTTCTTCCTGGAGCTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACCAAAGTGACCCGGATGCATG-----GAATCGACCCTGTGGTGCTGGTCCTGAT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCCGGCGCCCTCATGATGCTGGTGGGCTTCCTGGGCTGCTGCGGGGCTGTGCAGGAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCGGCCATCTGGGGATATTCCCACAAGGATGAGTGTATTAAGGAAGTCCAGGAGTTTTA 485
                                                                                                                                                                                                                                                                                                                                                                                                                               ROSELAND
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                    07068
                                                nucleic acid
                                                                   1344 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paul Moore, Reiner Gentz, Hongjin J
Jian Ni and Jing-Shan Hu
NYENTION: Human Genes, Sequences and
                                                                                                                            973-994-1744
                                                                                                                                                                                                                                                                                                                                                               IBM PS/2
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IMMEDIATE SOURCE:

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US-08-855-140-2
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastbEQ for Windows Version
                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: Herewith
                                                                                                              TELEPHONE: 415-855-0555
                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: NEW TRANSMEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          464 CACGGACAAGAT 475
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                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3174 POI
CITY: Palo Alto
          STRANDEDNESS:
                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                 FILING DATE:
TOPOLOGY:
                                        LENGTH:
                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                       nucleic acid
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                                         977
                                                                                                                                                                                                                                                                                                                                                                                                                          E: Incyte Pharmaceuticals, Inc
3174 Porter Drive
                                                                                                415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillman,
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linear
                                        base
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          single
                                        pairs
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52.6%;
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                                                                                                                                          PF-0296 US
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                                                                                                2.0
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US-08-855-140-2
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08807044 Patent No. 5863735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 248; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                        SOFTWARE: FASTSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hillman, Jenni
APPLICANT: Goli, Surya K.
                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 613 GGTTCCCGACCGCTGCTGCATGGAGAACTCCCAGGGC 649
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        553 GATGCGATGCTGTGTCTCACTGACTACACAGACTGGTACCCAGTGCTGGGGGAGAACAC
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                                     APPLICATION NUMBER: UFILING DATE: Herewith
                                                                                                                                                                                                                                           STREET: 3174 POCITY: Palo Alto
                                                                                                                                                                                                                                                 ADDRESSEE: Incyc- Drive
                   CLASSIFICATION:
                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGCGGTGCCAGCTACAGCCGAGAGAGAGTGCGGGGTC 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCCTACC-----GGGACGATATCGATCTGCAAAACCTCATCGACTCCCTTCAGAAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAACCAGTGCTGTGGCGCATATGGCCCTGAAGACTGGGACCTCAACGTCTACTTCAATTG
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                                                                                                                                                                                            94304
                                                                                                                                                                                                                               CA
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                                                                                                                                                                                                                                                                                    Incyte Pharmaceuticals, Inc
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48.0%;
                                                                                                                                                                                                                                                                                                                                                                              Jennifer L.
                                                                                                                                                                                                                                                                                                                                         NOVEL HUMAN TRANSMEMBRANE 4 SUPERFAMILY
                                                        US/08/807,044
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Pred. No. 2.9e-07;
0; Mismatches 257;
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                                                                                                                                                                                                                      Patent No. 6204000
GENERAL INFORMATION:
APPLICANT: Dong,
APPLICANT: J. Car
                                                                                                                                                                                                                                                                  Sequence 19, Application US/08430225A Patent No. 6204000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
          COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                              TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                 NUMBER OF SEQUENCES: Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: line IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 CAAGTACCTCCTTTTCAGCTACAACATCATCTTCTGGTTGGCTGGAGTTGTCTTCCTTGG 170
                                                                                                                                                                                                                                                                                                                                                  534 CACGGACAAGAT 545
                                                                                                                                                                                                                                                                                                                                                                             411 CCAGGACTGGGT 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                            STREET: 345 PARI
CITY: NEW YORK
STATE: NEW YORK
                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity hes 162; Conserv
                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: SCOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                       CCTGCTGCTGCTGGTGTTCCTGCTGGAGGCCACCATCGCCATCCTCTTCTTCGCCTA 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCCC----TGTCGGCTGCCAACCTGCTCATCATCACCGGCGCCTTTGTCATGGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAGTACCTCATGTTCGCCTTCAACCTGCTNTTCTGGCTGGGAGGCTGTGGCGTGCTGGG 299
                                                                  10154
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                                                                                                                         345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1151 base pairs
                                                                                                                                                                           J. Carl; Lamb, Patricia W.;
J. Carl; Lamb, Patricia W.;
VENTION: DIAGNOSTIC METHODS
VENTION: GENE THERAPY USING
VENTION: HUMAN METASTASIS SU
                                                                               USA
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WORDPERFECT
                                                                                                                                    MORGAN & FINNEGAN, L.L.P.
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51.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 61.4;
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                                                                                                                                                                              SUPPRESSOR
                                                                                                                                                                                                         AND
                                                                                                                                                                                           REAGENTS
                                                                                                                                                                                                                    Isaacs, John
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RESULT 13
US-08-807-044-4
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application Patent No. 5863735
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                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/807,044 FILING DATE: Herewith
                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                 APPLICANT: Hillman, Jen APPLICANT: Goli, Surya
                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1624 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
                                                                                                                                                                                            STREET: 31/1
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  492 CATGGGCAAGCTGAAGCAGGAGATGGGCGGCATCGT 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   411 CCAGGACTGGGTGAGGGACCGGTTCCGGGAGTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 AGTCGGGCTGTGGGCATGGAGCGAAAAGGGTGTGCTGTCCGACCTCACCAAAGTGACCCG 230
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                                                                                COMPUTER: IBM CONTROL OPERATING SYSTEM:
CLASSIFICATION:
                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                              ADDRESSEE: Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 3.9%;
Local Similarity 47.6%;
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TOPOLOGY: linear
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                                                                                                                                                                                                                            3174 Porter Drive
                                                                                                                                                                           USA
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(212) 751-6849
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                                                                                                  IBM Compatible
                                                                                                                       Diskette
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N: 514
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NOVEL HUMAN TRANSMEMBRANE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   446
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

FILING DATE:

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                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application PC/TUS9104986 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 415-855-0555
                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                           TITLE OF
                                                                                                                                                                                                                                            APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 TGGTCCTGATGGTGGGCGTGGTGATGTTCACCCTGGGGTTCGCCGGCTGCGGGGGCTC 316
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                                                                                    STREET: 5370 Mar
CITY: Boulder
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                        ADDRESSEE:
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                                                      80303
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                                                                                                                                                                                           INVENTION:
                                                                                                                     5370 Manhattan Circle, Suite 201
                                                                    USA
                                                                                                                                                                                                           Amiot, Martine
                                                                                                                                                                                                                       Stamenkovic, Ivan
Stengelin, Siegfried
                                                                                                                                                                                                                                                        Oquendo, Carmen
Simmons, David L.
                                                                                                                                                                                                                                                                                                         Camerini,
                                                                                                                                                                                                                                                                                                                         Aruffo, Alejandro
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                                                                                                                                                                                                                                                                                          Lauffer,
                                                                                                                                                                                                                                                                                                                                         Allen, Janet
                                                                                                                                                                                                                                                                                                                                                              Seed, Brian
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                                                                                                                                        Greenlee & Associates
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                                                                                                                                                                                       Rapid Immunoselection Cloning Method
                                                                                                                                                                                                                                                                                           Leander
                                                                                                                                                                                                                                                                                                           David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 52.8; DB 2;
Pred. No. 9.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 152;
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RESULT 15
US-09-020-956-16/c
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                                                                                                       Sequence 16, Application US/09020956 Patent No. 6261562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
              GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
APPLICANT: DILLIN, Davin C.
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 178
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/379,076
FILING DATE: 13-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 25-FEB-1988
ATTORNEY/AGENT INFORMATION:
NAME: Wall, Margaret M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 13-JUL-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

PRIOR APPLICATION UNMBER: US/07/553,759
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CORRESPONDENCE ADDRESS
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FILING DATE: 23-MAR-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                                                                                                                                                                                                                                                GGGAGTTCTTCGAGAGCAACATCAAGTCCTACCGGGACGATATCGATCTGCAAAACCTCA 496
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                                      FOR IMMUNOTHERAPY
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ADDRESSEE:

SEED and BERRY LLP

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; TOPOLOGY: 1;; MOLECULE TYPE: US-09-020-956-16
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FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAK!, DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
REFERENCE/DOCKET NUMBER: 210121.427C2
REFERENCE/DOCKET NUMBER: 10121.427C2
REFERENCE/DOCKET NUMBER: 10121.427C2
REFERENCE/DOCKET NUMBER: 110121.427C2
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,592
REFERENCE/DOCKET NUMBER: US/09/020,956
REFERENCE/DOCKET NUMBER: US/09/020,956
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REFERENCE/DOCKET NUMBER: US/09/020,956
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Search completed: December 19, 2002, 05:20:31 Job time : 63 secs
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Best Local Similarity
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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Minimum DB seq length: 0
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Perfect score:
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         US-09-905-674-1
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:/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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Listing first 45 summaries
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3 US-09-934-268-3

3 US-09-932-268-1

3 US-09-925-299-205

10 US-09-925-299-205

10 US-09-783-590-10353

9 US-09-875-440-1

10 US-09-784-873-12

10 US-09-764-873-12

12 US-10-052-586-277

12 US-10-042-417-37

10 US-09-764-873-14

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10 US-09-960-352-1269

10 US-09-985-888-307-2351

10 US-09-895-88-31

10 US-09-882-800-421

10 US-09-925-301-392

10 US-09-925-301-392

10 US-09-985-828-400

9 US-10-040-739-658
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3259.398 Million cell updates/sec
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              Sequence 3, Appli
Sequence 2, Appli
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Sequence 205, App
Sequence 10353, A
Sequence 169, App
Sequence 17, Appli
Sequence 277, Appl
Sequence 277, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 14, Appl
Sequence 18, Appl
Sequence 318, Appl
Sequence 318, Appl
Sequence 318, Appl
Sequence 317, Appl
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Sequence 319, Appl
Sequence 331, Appl
Sequence 332, Appl
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### ALIGNMENTS

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; LENGTH: 813
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-934-268-3
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Patent No. US20020172986A1
GENERAL INFORMATION:
APPLICANT: Leiby, Kevin R.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 515; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/934,268
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 60/226,612
PRIOR FILING DATE: 2000-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: 23228, A NOVEL HUMAN TETRASPANIN FAMILY TITLE OF INVENTION: MEMBER AND USES THEREOF FILE REFERENCE: 10448-079001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                      155 GAGTTGTCTTCCTTGGAGTCGGGCTGTGGGCGATGGAGCGAAAAGGGTGTGCTGTCCGACC 214
                                                                                                                                                                                                                                                                                                                                                                    95 AAGTCAGCTGCTGGTACAAGTACCTCCTTTTCAGCTACAACATCATCTTCTGGTTGGCTG 154
                                                                         TGGTGATGTTCACCCTGGGGTTCGCCGGCTGCGGGGGGGCTCTGCGGGGGAGAATATCTGCT 334
                                                                                                                                                                         TCACCAAAGTGACCCGGATGCATGGAATCCGACCCTGTGGTGCTGGTCCTGATGGTGGGCG
GCGTCATGTCGGTGCTGGGCTTTGCTTGGCTGCATTGGGGCCCTCCGGGAGAACACCTTCC
                                                                                                                                             TCTCAGCGCTGACAGATCTGGGAGGCCTTGACCCCGTGTGGCTGTTTGTGGTAGTTGGAG
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                                                                                                                                                                                                                                          GAGCCCTGTTCCTGGCTATCGGCCTCTGGGCCTGGGGTGAGAAGGGCGTTCTCTCGAACA 154
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TITLE OF INVENTION: 23228, A NOVEL HUMAN TETRASPANIN FAMILY
TITLE OF INVENTION: MEMBER AND USES THEREOF
FILE REFERENCE: 10448-079001
CURRENT APPLICATION NUMBER: US/09/934,268
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 60/226,612
PRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO
TYPE: DIA
OPENITSM. USED GENERAL
OPENITS
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                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 515; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Leiby, Kevin R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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      TCACCAAAGTGACCCGGATGCATGGAATCGACCCTGTGGTGCTGGTCCTGATGGTGGGCG
                                                                     GAGCCCTGTTCCTGGCCTATCGGCCTCTGGGCCTGGGGTGAGAAGGGCGTTCTCTCGAACA
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            GCATCTTCCTGGCAAGGACGCTGATCTCAGACATCGAGGCAGTGAAGGCC 864
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                                                  TGGAGCAGCAGGGCTTCATCCACACCAAAGGCTGCGTGGGCCAGTTTGAGAAGTGGCTGC
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GCATCTGCCTGGCCCAGAACCTCGTGAGTGACATCAAGGCAGTGAAAGCC
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; TYPE: DNA
; ORGANISM: Homo sapiens
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                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09972970 Patent No. US20020164693A1
                                                                                Matches
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/972,970
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: PCT/US01/11130
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,336
PRIOR EPILING DATE: 2000-04-10
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Shi et al.
TITLE OF INVENTION: TM4SF Receptor Polynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: PT056P1
                                                                                                                                                                                                                                  LENGTH: 2538
150 CCGAGGTCGGCTGCGGGGAAATACTTCCTGTTTGGCTTCAACATTGTTTTCTGGGTGC
                                      92 CCAAAGTCAGCTGCTGGTACAAGTACCTCCTTTTCAGCTACAACATCATCTTCTGGTTGG 151
                                                                                   Conservative
                                                                                                       25.3%;
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                                                                                   Score 351.8; DB 9;
Pred. No. 3.4e-85;
0; Mismatches 252;
                                                                                                                           Length
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CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 205
LENGTH: 1655
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US-09-925-299-205
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                                                                                                                                                                                                                          Sequence 205, Application US/09925299 Patent No. US20020055627A1 GENERAL INFORMATION:
                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA102
NAME/KEY: misc_feature LOCATION: (1548)
                         FEATURE:
                                     ORGANISM: Homo sapiens
                                                   TYPE: DNA
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; NAME/KEY: misc_feature
; LOCATION: (1643)
; OTHER INFORMATION: n ec
US-09-925-299-205
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Best Local Similarity
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NAME/KEY: misc_feature
LOCATION: (1559)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
LOCATION: (1564)
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OTHER INFORMATION: n equals
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                                                                                                                                        AGATCCTGCGCAAAAAGTTGTGAACACACAGTGTGGGATATGATGTCAGGATTCAGCTGAA
                                                                                                                                                                        TIGCACAGATICCAATGCAAGTCGAGAGCGATGTGGCGTTCCATTCTCCTGCTGCACTAA
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                                   GCAGGACAATTTAACCATCGTTGCTGGTATTTTCATAGGCATTGCATTGCTGCAGATATT
                                               CCCGCGGAACATTTACATTGTGGCTGGCGGCTCTTCATCGCCATCTCGCTGTTGCAGATATT
                                                                                         GAGCAAGTGGGATGAGTCCATCTTCACGAAAGGCTGCATCCAGGCGCCTGGAAAGCTGGCT
                                                                                                                           ATATTGGCAGTGCTGTGGGGCTTTTGGAGCTGATGATTGGAACCTAAATATTTACTTCAA
                                                                             AGTTGACCAGCAGATTGTAATCTACACGAAAGGCTGTGTGCCCCAGTTTGAGAAGTGGTT
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pred. No. 2.2e-81;
0; Mismatches 311;
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APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and
FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR FILING DATE: 1995-04-12
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COCATION: (5)
OTHER INFORMATION: n equals a,
NAME/KEY misc feature
LOCATION: (195)
OTHER INFORMATION: n equals a,
NAME/KEY misc feature
LOCATION: (285)
OTHER INFORMATION: n equals a,
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10353, Application US/09783590 Patent No. US20020110850A1 GENERAL INFORMATION:
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-09-783-590-10353
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APPLICANT: Haseltine, Willia
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
                                                                                                               IOCATION: (400)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
                                                           LOCATION: (408)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
LOCATION: (411)
                                            OTHER INFORMATION: n equals
                                                                                                                                                             LOCATION: (394)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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LOCATION: (314)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (324)
                            NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                   LOCATION: (340)
OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g, or
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   INFORMATION: n
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                                                                                                 Matches
                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1

LENGTH: 864

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09875440 Patent No. US20020156035A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 342; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Winter, Jill A.
APPLICANT: Randazzo, Filippo
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                                                                                               Conservative
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                                                                                                            16.6%;
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87.9%;
                                                                                              Score 230; DB
Pred. No. 1.5e
0; Mismatches
                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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; OTHER INFORMATION: NET-4 oligonucleotide used in ; OTHER INFORMATION: assay on SW620 cells US-09-875-440-1
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: MEDPLASTIC DISEASE USING NET-4 MODUL!
EILE REFERENCE: PP-01701.002/200130.522
CURRENT APPLICATION NUMBER: US/09/875,440
CURRENT FILING DATE: 2001-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     747 CTGGCTCCCGCGG-AACATTTACATTGTGGCTGGCGTCTTCATCGCCATCTCGCTGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          687 GCTGAAGAGCAAGTGGGATGAGTCCATCTTCACGAAAGGCTGCATCCAGGCGCCTGGAAAG 746
CAAAGTCAGCTGCTGGTACAAGTACCTCCTTTTCAGCTACAACATCATCTTCTGGTTGGC 152
                                                           GCTGCCGGGGCAAGTGTCTTCATGAACCCAGAGGATGTCCGGGAAGCACTACAAGGGTCC 373
                                                                                              GCCGCCGCCGCGCGCATTCTGCTTCTCAGAAGATGCACTATTATAGATACTCTAACGC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGTGCCCCATC-TTAAGCATCAGCGTGA----CGTGACCTCTCTGTTTCTGCTTGCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGCTCCCGCGGTAACATTTACATTGTGGCTGGCGTCTTCATCGCCATCTCGCTGTTGC
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Pred. No. 6e-57;
D; Mismatches 37;
                                                                                                                                                              DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NET-4 MODULATORS
                                                                                                                                                                                                                                                        cell proliferation
                                                                                                                                                                              Length 864;
                                                                                                                                         Indels
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                                                                                                     ; TYPE: DNA; ORGANISM: Homo sapiens US-09-729-674-169
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APPLICANT: MCCOy, John M.
APPLICANT: LaVallie, Edward
APPLICANT: Collins-Racie, L
APPLICANT: Evans, Cheryl
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Murice
APPLICANT: Steininger II, R
APPLICANT: Steininger II, R
                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 169
LENGTH: 1110
                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 169, Application US/09729674 Patent No. US20010039335A1
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
                                                                                                                                                                                                                                                                                                APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          854
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                                 Local Similarity les 477; Conserv
 33 GCCGCCGCCGCGCGCGTTCTGCTTCTCAGAAGATGCACTATTATAGATACTCTAACGC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAACATCAAGTCCTACCGGGACGATATCGATCTGCAAAACCTCATCGACTCCCTTCAGAA
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Treacy, Maurice
Agostino, Michael J.
Steininger II, Robert J.
Spaulding, Vikki
Wong, Gordon G.
Clark, Hilary
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LaVallie, Edward R.
Collins-Racie, Lisa /
Evans, Cheryl
                                   Conservative
                                                  16.5%;
57.1%;
                                Score 229; DB 10;
Pred. No. 3.1e-52;
2; Mismatches 292;
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                                                                 Length 1110;
                                 Indels
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                                                                                                               738 AGTTGACCAGCAGATTGTAATCTACACGAAAGGCTGTGTGCCCCCAGTTTGAGAAGTGGTT
                                                                                                                                                                                      633 AGATCCTGCGCAAAAAGTTGTGAACACACAGTGTGGATATGATGTCAGGATTCAGCTGAA
                                                                                                                                                                                                                                              573 TTGCAGCGGTGCCAGCTACAGCCGAGAGAGAGTGCGGGGTCCCCTTCTCCTGCTGCGTGCC
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                                                       GAGCAAGTGGGATGAGTCCATCTTCACGAAAGGCTGCATCCAGGCGCTGGAAAGCTGGCT
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US-09-764-873-12
Sequence 12, Application US/09764873
Patent No. US20029151479A1
GENERAL INFORMATION:
              Prior application data removed -
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 545
TYPE: DNA
TYPE: DNA
                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/764,873
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                   APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ01
ORGANISM: Homo sapiens
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                                                                                                                                   or file wrapper
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Antibodies

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APPLICAMN: TOOL, MILLIAM 1.

APPLICAMN: Zhang, Zemin 1.

APPLICAMN: Zhang, Zemin 1.

APPLICAMN: Zhang, Zemin 1.

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3430RIC1

CURRENT EPILME DATE: 2002-01-15

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/05926

PRIOR APPLICATION NUMBER: 60/05926

PRIOR APPLICATION NUMBER: 60/05250

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/06320

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/06312

PRIOR APPLICATION NUMBER: 60/06312

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/06312

PRIOR APPLICATION NUMBER: 60/06340

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/06340

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/06354

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/06354

PRIOR APPLICATION NUMBER: 60/06354

PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/06354

PRIOR APPLICATION NUMBER: 60/06364

PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/06364

PRIOR APPLICATION NUM
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US-10-052-586-277
Sequence 277, Application US/10052586
Patent No. US20020127584A1
GENERAL INFORMATION:
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Godowski, Paul J
Gurney, Austin L
Pan, James
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith, Victoria
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OR APPLICATION NUMBER: 60/080194
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OR APPLICATION NUMBER: 60/080327
OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/080333
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OR APPLICATION NUMBER: 60/081049
OR APPLICATION NUMBER: 60/081070
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OR APPLICATION NUMBER: 60/069335
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OR APPLICATION NUMBER: 60/069425
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FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/083495
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FILING DATE: 1998-03-10
APPLICATION NUMBER: 60/077632
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APPLICATION WITHOUT
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083559
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FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082704
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APPLICATION NUMBER: 60/079664
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079786
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FILING DATE: 1998-05-06
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OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088866
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                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: PAGANO, M.
APPLICANT: PAGANO, M.
TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT
TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
FILE REFERENCE: 5914-090-999
                                                                         SOFTWARE: PatentIn Ver. SEQ ID NO 37
                                                                                                                                                                                                                                                              Sequence 37, Application US/10042417 Patent No. US20020123082A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                  CURRENT FILING DATE: 2002-01-07
                                                                                                                     PRIOR APPLICATION NUMBER: 60/260,179 PRIOR FILING DATE: 2001-01-5
                                                                                                        NUMBER OF SEQ ID NOS: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/
                           ORGANISM: Homo sapiens
NAME/KEY: modified_base
                FEATURE:
                                               TYPE:
                                                            ENGTH:
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-873-14
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US-09-764-873-14
GENERAL INFORMATION:
APPLICANT: Wairen, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ01
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Best Local Similarity
Matches 110; Conserv
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Patent No. US20020151479A1
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Best Local Similarity
                                                                                                                                          Sequence 1269, Application US/09960352 Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/764,873
CURRENT FILING DATE: 2001-01-17
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Pred. No. 2.8e-21;
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Pred. No. 6.3e-20;
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APPLICANT: Wang, Tongtong
APPLICANT: McNeill, Patricia D.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.539
CURRENT APPLICATION UNMBER: US/09/895,828
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 473
COMPMENDE: FORFICE OF SEC. 10.
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; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 06-LIB3058-036-Q1-K1-B5
US-09-960-352-1269
                                                  ; OTHER INFORMATION: n = US-09-895-828-318
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CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 1269
                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 318
LENGTH: 547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 318, Application US/09895828 Patent No. US20020099012A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
              Query Match
                                                                                     NAME/KEY: misc_feature LOCATION: 4, 5
                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                        FEATURE:
                                                                                                                                                              TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90
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53.1%;
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Score
Pred.
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Pred. No. 4.4e-10;
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69.8;
No. 1.
DB 10;
.9e-09;
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Best Local Similarity

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CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2351
SEQ ID NO 2351
LENGTH: 1192
                                                                                                                                                                                                                                        ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M38690 US-09-880-107-2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-09-880-107-2351
; Sequence 2351, Application US/09880107
; Patent No. US20020142981A1
                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT: Vockle
APPLICANT: Scherf
APPLICANT: Gene L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-WO
                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                            FEATURE:
         186
                           216 CACCAAAGTGACCCGGATGCATG-----GAATCGACCCTGTGGTGCTGGTCCTGAT---
                                                                               156 AGTTGTCTTCCTTGGAGTCGGGCTGTGGGGCATGGAGCGAAAAGGGTGTGCTGTCCGACCT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 AGTTGTCTTCGTTGGAGTCGGGCTGTGGGGCATGGAGCGAAAAGGGTGTGCTGTCCGACCT
                                                                                                                    66 AGGCACCAAGTGCATCAAATACCTGCTGTTCGGATTTAACTTCATCTTCTGGCTTGCCGG 125
                                                                                                                                                                                   Local Similarity
nes 199; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 GATTGCTGTCCTTGCCATTGGACTATGGCTCCGATTCGACTCTCAGACCAAGAGCATCTT
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 CGAGCAAGAAACTAATAATAATTCCAGCTTCTACACAGGAGTCTATATTCTGATCGG
                                                          GATTGCTGTCCTTGCCATTGGACTATGGCTCCGATTCGACTCTCAGACCAAGAGCATCTT
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                                                                                                                                                                                           Score 69.8; DB 10;
Pred. No. 2.7e-09;
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                                                                                                                                                                                Mismatches 167;
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LENGTH: 1219
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                         Matches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: HOMO
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Clark, Hilary
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                                                                                                                                                                                                                                                                                                                                                      Conservative
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Sequence 421, Application US/09822830A Patent No. US20020142952A1
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APPLICANT: Gulukota, Kamalakar
APPLICANT: Grahan, James R.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6402
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,604
                                           387 TGTGGCCGTGCTTGCCTGTTCCAGGACTGGGTGAGGGACCGGTTCCGGGAGTTCTT
                                                                                                                                                                                                                                                                                                                                            216 CACCAAAGTGACCCGGATGCATG-----GAATCGACCCTGTGGTGCTGGTCCTGAT---
                                                                                                                                                                                                                                                                                                                                                                                                                                           156 AGTTGTCTTCCTTGGAGTCGGGCTGTGGGCATGGAGCGAAAAGGGTGTGCTGTCCGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387 TGTGGCCGTGCTGGCCTTCCTGTTCCAGGACTGGGTGAGGGACCGGGTTCCGGGAGTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306 CCAGTGCATGCTGGGACTGTTCTTCGGCTTCCTCTTGGTGATATTCGCCATTGAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 AGTCAGCTGCTACAAGTACCTCCTTTTCAGCTACAACATCATCTTCTGGTTGGCTGG 155
                                                                                                 CCAGTGCATGCTGGGACTGTTCTTCGGCCTTCCTTTGGTGATATTCGCCATTGAAATAGC
                                                                                                                           TATCTGCTTGCTCAACTTTTTCTGTGGCACCATCGTGCTCATCTTCTTCCTGGAGCTGGC
                                                                                                                                                                                                                                          GGTGGGCGTGGTGATGTTCACCCTGGGGTTCGCCGGCTGCGTGGGGGGCTCTGCGGGAGAA 326
TGCGGCCATCTGGGGATATTCCCCACAAGGATGAGGTGATTAAGGAAGTCCAGGAGTTTTA
                                                                                                                                                                                                 AGCCGGCGCCTCATGATGCTGGGCTTCCTGGGCTGCTGCGGGGCTGTGCAGGAGTC
                                                                                                                                                                                                                                                                                             CGAGCAAGAAACTAATAATAATTCCAGCTTCTACACAGGAGTCTATATTCTGATCGG
                                                                                                                                                                                                                                                                                                                                                                                               GATTGCTGTCCTTGCCATTGGACTATGGCTCCGATTCGACTCTCAGACCAAGAGCATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGCACCAAGTGCATCAAATACCTGCTTCGGATTTAACTTCATCTTCTGGCTTGCCGG
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Page 10

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-O-/Cgn2_1/USPTO_Spool/US09905674/runat_16122002_111845_6756/app_query.fasta_1.455
-O-/Cgn2_1/USPTO_Spool/US09905674/runat_16122002_111845_6756/app_query.fasta_1.455
-DB=GenEmbl -OFMT-fastap -SUFFIX=-yge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=20000000000
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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<pre>rpSerGluLysGlyValLeuSerAspLeuThrLysValThrArgMetHisGlyIleAsp 60  </pre>	AGCTACAACATCATCTTCTGGTTGGCTGGAGTTGTCTTCCTTGGAGTCGGGCTGTGGGCA 192	erTyrAsnIleIlePheTrpLeuAlaGlyValValPheLeuGlyValGlyLeuTrpAla 40	MetHisTyTTyrArgTyrSerAsnAlaLysValSerCysTrpTyrLysTyrLeuLeuPhe 20 	674-2 (1-270) x AF311903 (1-2553)	Internation	/COUCH_Scall=1 /PICOUCH_Scall=1 /PICOUCH	/organism="Homo sapiens" /db_xref="taxon:9606" 73	Location/Qual 12553	ssion 6-OCT ersit	2553)	Zhang, W., Li, N., Wan, T. and Cao, X.  Identification of novel membrane proteins	nomo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2553)	000	Homo sapiens DC-TM4F2 precursor, mRNA, complete cds. AF311903.1 GI:22266721	$\mathcal{C}_{N}\mathcal{A}_{N}\mathcal{A}_{N}$ disconnected the description of the contract of the contr	ATCGAGGCAGTGAAGGCCGGCCATCACTTC 876	lleGluAlaValLySAlaGlyHisHisPhe 270	ATCGCCATCTCGCTGTTGCAGATATTTGGCATCTTCCTGGCAAGGACGCTGATCTCAGAC 846	ileAlaileSerLeuLeuGlnIlePheGlyIlePheLeuAlaArgThrLeuIleSerAsp 260	CyslleGlnAlaLeuGluSerTrpLeuProArgAsnIleTyrIleValAlaGlyValPhe 240	

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                                                                                                                                                                                                                                                                                                               Homo sapiens complete cds. AL136638
                                                                        Submitted (10-JUL-2002) GSF, Institut fuer Bioinformatik MIPS, Ingolstaedter Landstr. 1, 85764 Neuherberg, Germany Clone from S. Wiemann, Molecular Genome Analysis, German Cance Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of t German Genome Project.
 Berlin-Charlottenburg, GERMANY; Finformation about the clone and t at http://mips.gsf.de/proj/cDNA/
                                             This clone (DKFZp564B1037) is available at the Please contact the RZPD: Ressourcenzentrum, Heu
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 2556)
Poustka,A., Klein,M., Mewes,H.W., Gassenhuber,J. and
Direct Submission
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DKFZp564B1037 (
                Ressourcenzentrum, Heubnerwe
ERMANY; Email: clone@rzpd.de
one and the sequencing projec
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                                    GlnAsnLeuIleAspSerLeuGlnLysAlaAsnGlnCysCysGlyAlaTyrGlyProGlu
                                                                    SerTyrAsnIleIlePheTrpLeuAlaGlyValValPheLeuGlyValGlyLeuTrpAla
AspTrpAspLeuAsnValTyrPheAsnCysSerGlyAlaSerTyrSerArgGluLysCys
                       CAAAACGTCATCGACTCCCTTCAGAAAGCTAACCAGTGCTGTGGCGCATATGGCCCTGAA
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gylsdlfkvtrhhgidbyvlvlmvgvvmetlofagcvgalrenicllnfecctivlif
flelavavlaflgomvrdrereffesniksyrddidlonvidslokanoccaygep
dwdlnvyfncsgasysrekcgvpfsccvpdpaokvvntogcgvdvriolkskwdesift
kgciqaleswlprnixivagvftaislloifgiflartlisdieavkagrhf"
2546
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/tissue_type="brain"
/clone_lib="564 (synonym: hfbr2).
X1-2blue; sites NotI + SalI"
/dev_stage="fetal"
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/protein_id="CAB66573.1
/db_xref="GI:12052802"
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/codon_start=1
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/db_xref="taxon:9606"
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BC025568.1
MGC.
                                                                           Clone distribution: MGC clone distribution informat through the I.M.A.G.E. Consortium/LIMI at: http://i Series: IRAK Plate: 56 Row: j Column: 21 This clone was selected for full length sequencing passed the following selection criteria: GenomeScar
                                                                                                                                                                      Contact: nisc_mgc@nhgri.nih.gov

Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,

Maduro,C.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramur Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 2428)
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/organism="Mus musculus"
/db_xref="taxon:10090"
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US-09-905-674-2 (1-270) x BC025568
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                                                                                          GlyValProPheSerCysCysValProAspProAlaGlnLysValValAsnThrGlnCys
                                                                                                                                                                                                                                         CAGAACCTCATTGACTCCCTTCAGAAAGCTAATCAGTGCTGCGGGGGCTTACGGCCCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                          GlnAsnLeuTleAspSerLeuGlnLysAlaAsnGlnCysCysGlyAlaTyrGlyProGlu
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                                                                                                                                                     GACTGGGACCTCAATGTCTACTTCAACTGCAGTGGTGCCAGCTACAGCCGAGAGAAATGT
                                                                                                                                                                              AspTrpAspLeuAsnValTyrPheAsnCysSerGlyAlaSerTyrSerArgGluLysCys
                                                                                                                                                                                                                                                                                                                             GACCGGTTCCGGGAATTCTTCGAGAGCAACATCAAGTCCTATCGGGATGACATCGACCTG
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                                                                    GGGGTACCCTTCTCCTGCTGTGTGCCAGATCCTGCACAAAAAGTCGTGAACACACAGTGT
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GVLSDLTKVTRLHGIDPVLVLWWGVVMFTLGEAGCVGALEBNICLLKEFCGAIVLIF
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DWDLLNYFNCSGASYSREKGGVPFSCCVPDPAQKVVNTQCGYDYRIQLKSKWDEFIFT
KGCIQALEGWLFRNIYIVAGVFIAISLLQIFGIFLARTLISDIEAVKAGHHF"

640 c 624 g 647 t
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ductal carcinoma. 5 month old virgin mouse."
/clone_lib="NCI_CGAP_Mam6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product "Similar to region containing protein MGC11352; slingshot" /protein id-"AAH25568 l" /db_xref="GI:19343884"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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BC024611.1
MGC.
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MGC11352;
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This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly)
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (01-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 2498)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Richards, S., Gibbs, R.A.
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/translation="mhyyrysnaevscwykyllesynivfwlagvvflgvglwawsek
gvlsdltkvTrlhgidpvvlvlwvgvvmfTlgFagcvgalrenicllkffcgaivlif
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/clone_lib="NCI_CGAP_SG2"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                 /codon_start=1
                                                                                                                                                    /note="Vector: pCMV-SPORT6"
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S., Martin,
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                                                                                            hypothetical
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BASE CO	FLEIAVAVLAFLFQDWVRDRFREFFESNIKSYRDDIDLQNLIDSLQKANQCCGAYGPE DWDLNVYFNCSGASYSREKCGVPFSCCVPDPAQKVVVNTQCGYDVRIQLKSKWDEFIFT KGCIQALEGWLPRNIYIVAGVFIAISLLQIFGIFLARTLISDIEAVKAGHHF" 542 a 644 c 631 g 681 t
Alignman Pred.   Score: Score: Percen: Best Language Query   DB:	nment Scores:       2.58e-150       Length:       2498         1. No.:       1.420.00       Matches:       263         ee:       1.528       Conservative:       3         cocal Similarity:       97.418       Mismatches:       4         y Match:       98.008       Indels:       0         Gaps:       0       Gaps:       0
US-09-	905-674-2 (1-270) x BC024611 (1-2498)
Qу Db	1 MethisTyrTyrArgTyrSerAsnAlaLysValSerCysTrpTyrLysTyrLeuLeuPhe 20
Oy	21 SerTyrAsnIleIlePheTrpLeuAlaGlyValValPheLeuGlyValGlyLeuTrpAla 40
Фр	41 TrpSerGluLysGlyValLeuSerAspLeuThrLysValThrArgMetHisGlyIleAsp 60
P Q	61 ProValValLeuValLeuWetValGlyValValMetPheThrLeuGlyPheAlaGlyCys 80 
Δδ .:	81 ValGlyAlaLeuArgGluAsnIleCysLeuLeuAsnPhePheCysGlyThrIleValLeu 100
Qγ Tb	101 IlePhePheLeuGluLeuAlaValAlaValLeuAlaPheLeuPheGlnAspTrpValArg 120 
D <sub>0</sub> Δ <sub>γ</sub>	121 AspArgPheArgGluPhePheGluSerAsnIleLysSerTyrArgAspAspIleAspLeu 140 
Qy :	141 GlnAsnLeuTleAspSerLeuGlnLysAlaAsnGlnCysCysGlyAlaTyrGlyProGlu 160 
Qγ .:	161 AspTrpAspLeuAsnValTyrPheAsnCysSerGlyAlaSerTyrSerArgGluLysCys 180 
φ :	181 GlyValProPheSerCysCysValProAspProAlaGlnLysValValAsnThrGlnCys 200 
Qу :	201 GlyTyraspValargIleGlnLeuLysSerLysTrpAspGluSerIlePheThrLysGly 220 
Db Qy	221 CysileGinAlaLeuGluSerTrpLeuProArgAsnIleTyrIleValAlaGlyValPhe 240 
D 04	241 IleAlaIleSerLeuLeuGlnIlePheGlyIlePheLeuAlaArgThrLeuIleSerAsp 260 
P 04	261 IleGluAlaValLysAlaGlyHisHisPhe 270 
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BC026574
LOCUS
DEFINITION
ACCESSION
VERSION
· KEYWORDS
SOURCE
ORGANISM
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Best Local Similarity:
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 50
               MetHisTyrTyrArgTyrSerAsnAlaLysValSerCysTrpTyrLysTyrLeuLeuPhe
ATGCACTATTATAGATACTCGAACGCCGAGGTCAGCTGCTGCTGCTACAAGTACCTGCTCTTC
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This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@nail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-APR-2002) National Institutes of Health, Mammaliar Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC026574 2500 k
Mus musculus, clone MGC:36554
BC026574 GI:20072352
MGC.
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Mus musculus
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R. M.
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                                                                                                                                                                                                                                                 /translation="MHYYRYSNAEVSCWYKYLLFSYNIVFWLAGVVFLGVGLWAWSEK GVLSDLTKVTRLHGIDPVLYLMVGVVMETLGFAGCVGALREBICLLKFTCGAIVLIF FLELAVAVLAFLFQDWVDLDFREFFESNIKSYDDIDLQMLIDSLQKANQCCGAYGPE DWDLLAVYFNCSGASYSREKGGVPFSCCVPDPAQKVVNTQCGYDVRIQLKSKWDEFIFT KGCIQALEGWLPRNIYIVAGVFIAISLLQIFGIFLARTLISDIEAVKAGHF" 643 c 631 g 681 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="MGC:36554 IMAGE:4954874"
/tissue_type="Mammary tumor. C3(1)-Tag model.
ductal carcinoma. 5 month old virgin mouse."
/clone_lib="NCI_CGAP_Mam6"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                     /product="Unknown (protein for MGC:36554)"
/protein_id="AAH26574.1"
/db_xref="GI:20072353"
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/db_xref="taxon:10090"
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Submitted (05-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                  BC002920 2502 bp mRNA linear I Homo sapiens, Similar to transmembrane 4 superfamily clone MGC:11352 IMAGE:3954042, mRNA, complete cds.
                                             Direct Submission
                                                           Strausberg, R.
                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                         Homo sapiens
                                                                                                                                                                     BC002920.1
                                                                                         Mammalia;
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                                                                          (bases 1 to 2502)
                                                                                                                                                                      GI:12804132
                                                                                          Chordata;
Primates;
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                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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NIH-MGC Project URL: http://mgc.nci.nih.gov

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Query Match:
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                                                                          ATGCACTATTATAGATACTCTAACGCCAAGGTCAGCTGCTGCTACAAGTACCTCCTTTTC
    ValGlyAlaLeuArgGluAsnIleCysLeuLeuAsnPhePheCysGlyThrIleValLeu
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Contact: nisc_mgc@nhgri.nih.gov/
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://lnage.llnl.gov Series: IRAL Plate: 15 Row: e Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland, Washersburg, Maryland, Washersburg, Maryland, Washersburg, Maryland, Washersburg, Washersb
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Tissue Procurement: ATCC/DCTD/DTP
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/product="Similar to transmembrane 4 superfamily member 9"
/protesin_id="AAH02920.1"
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RDRFREFFESNIKSYRDDIDLOWLIDSLQKANQCCGAYGPEDWDLNVYENCSGASYSR
EKGGVPFSCCVPDPAQKVVNTQCGYDVRIQLKSKWDESIFTKGCIQALESWLPRNIYI
VAGVFIAISLLQIFGIFLARTLLSDIEAVKAGHHF"

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/db_xref="taxon:9606"
/clone="mGC:11352 IMAGE:3954042"
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/lab_host="DH10B-R"
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                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1405)
                                                                                                                                                                                                                                                Serru, V., Dessen, P., Boucheix, C. and Rubinstein, E. Sequence and expression of seven new tetraspans Biochim. Biophys. Acta 1478 (1), 159-163 (2000) 20185353
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AF065389.1
                                                                                                                                                                 Submitted (14-MAY-1998) INSERM U268, Villejuif 94807, France
                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                       Rubinstein, E., Serru, V.
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens tetraspan NET-4 mRNA,
                                                                                                                                                                                                                                    10719184
                                                                                                                                                                                                                    (bases 1 to 1405)
/product="tetraspan NET-4"
/protein_id="AAC17120.1"
/db_xref="GI:3152703"
/translation="MSGKHYKGPEVSCCIKYFIFGFNVIFWFLGITFLGIGLWAWNEK
                                                                                  348. .1154
                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE ID 219547"
                                                                                                                                                  Location/Qualifiers
                                                                   /note="similar to Tspan-5;
                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                        GI:3152702
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Euteleostomi;

PRI 29-OCT-2001 clone MGC:9300

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US-09-905-674-2 (1-270) x AF065389 (1-1405)
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                                                                                                                             LeuGlnIlePheGlyIlePheLeuAlaArgThrLeuIleSerAspIleGluAlaValLys
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                                                                                                                                                                                                                                                                CAAAAACCAGAAGTTGACCAGCAGATTGTAATCTACACGAAAGGCTGTGTGCCCCCAGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerLeuGlnLysAlaAsnGlnCysCysGlyAlaTyrGlyProGluAspTrpAspLeuAsn 165
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FLELTAGVLAFVKDWIKDQLVFFINNNIRAYRDDIDLQNLIDETQEYWQCCGAFGAD
DWNLNIYFNCTDSNASRERGGVPFSCCTKDPAEDVINTQCGYDARQKPEVDQQIVIYT
KGCVPQFEKWLDDNLTIVAGIFIGIALLQIFGICLAQNLVSDIEAVRASW*
a 357 c 387 g 352 t
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                      TyrSerAsnAlaLysValSerCysTrpTyrLysTyrLeuLeuPheSerTyrAsnIleIle
TACAAGGGTCCTGAAGTCAGTTGTTGCATCAAATACTTCATATTTGGCTTCAATGTCATA
                                                                                                                                                                                                                                             Scores:
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 3152 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, Web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (29-JUN-2001) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
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                                                                                                                                                                                                                                                                                                    /product="transmembrane 4 superfamily member 9"
/protein_id="AAH09704.1"
/db_xref="Gi:16307231"
/translation="MSGKHYKGPEVSCCIKYFIFGFNVIFWFLGITFLGIGLWAWNEK
GVLSNISSITDLGGFDPWLFLVVGGVMFILGFAGCIGALRENTFLLKFFSVFLGIIF
ELELTAGVLAFVKDWIKDQLYFFINNNIRAYRDDIDLONLIDFTQEYWQCGAFGAD
DWNLNIYFNCTDSNASRERGGVPFSCCTKDPAEDVINTQCGYDARQKPEVDQQIVIYT
KGCVPQFEKWLDDNLTIVAGIFIGIALLQIFGICLAQNLVSDIEAVRASW"
a 354 c 385 g 352 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="LocusID:56224"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH10B"
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/clone_lib="NIH_MGC_70"
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                                                                                                                      3.81e-88
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Mus musculus

Ekkaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Rodentia; Sc
1 (bases 1 to 3175)

Garcia-Frigola,C., de Lecea,L. a
Mouse Tspan-5 CDNA cloning
Unpublished
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Mus musculus
AF121344
AF121344.1 G
Direct Submission
Direct Submission
Submitted (20-JAN-1999) Dept. of Animal and Plant
Submitted (20-JAN-1999) Av. Diagonal 645, Barcelo
                                       2 (bases 1 to 3175)
Garcia-Frigola, C., d
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Sciurognathi; Muridae;
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     Cell Biology,
ona 08028, Spain
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IleGlnLeuLysSerLysTrpAspGluSerIlePheThrLysGlyCysIleGlnAlaLeu
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                                                                                             ATTTACTTCAATTGCACAGATTCCAATGCAAGCCGAGAGCGATGCGGTGTGCCATTTTCC
                                                                                                             ValTyrPheAsnCysSerGlyAlaSerTyrSerArgGluLysCysGlyValProPheSer
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/product="tetraspanin Tspan-5"
/product="de"aA#28869.1"
/protein_id="AA#28869.1"
/db_xref="GI-6841033"
/db_xref="GI-6841033"
/db_xref="GI-686K1YK6PEVSCCIKYFIFGENVIFWFLGITELGIGLMAWNEK
/translation="MSGK1YKEPEVSCOIKYFIFGENVIFWFLKFFSVFLGIIF
GPLSNISSITDLGGFDPWLFLVVGGVMFILGFAGCIGALRENTFLLKFFSVFLGIIF
FLELTAGVLAFVFKDWIKDQLYFFINNITAAVADDIDLONLIDFTQEYWQCCGAFGAD
DWNLNIYFNCTDSNASRERCGVPFSCCTKDPAEDVINTQCGYDARQKPEVDQIVIYT
KGCVPQFEKWLDDNLTIVAGIFIGIALLQIFGICLAQNIVSDIEAVRASW"
a 811 c 840 g 857 t
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/codon_start=1
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/strain="Swiss Webster/NIH"
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MGC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Hump
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (05-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                             Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BC010346 1516 bp mRNA Mus musculus, RIKEN cDNA 2210021G21 gene, IMAGE:2811935, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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old, gross tissue."
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                                                                                                                                                                                                                                                /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                        CCCTTCTCCTGCTGCGTCAGGGACCCTGCGGAGGATGTCCTCAACACCCAGTGTGGCTAC
                                                                ProPheSerCysCysValProAspProAlaGlnLysValValAsnThrGlnCysGlyTyr
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Location/Qualifiers
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Todd, S.C., Doctor, V.S. and Levy, S. Sequences and expression of six new members tetraspanin/TM4SF family
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9714763
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Homo sapiens tetraspan
AF053455
                                                                                                             Submitted (12-MAR-1998) Medicine, Stanford, CA 94305, USA
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Todd, S.C., Doctor, V.S.
Direct Submission
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352. .1146
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352. .1146
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CTGCAGATATTTGGGATATGCCTGGCCCAGAATTTGGTTAGCGATATCGAAGCTGTCAGG
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                                                                                                                                          CAAAAACCAGAAGTTGACCAGCAGATTGTAATCTACACGAAAGGCTGTGTGCCCCAGTTT
                                                                                                                                                                                                                                                                                                                                                          TTCACCCAGGAATATTGGCAGTGCTGTGGGGCTTTTGGAGCTGATGATTGGAACCTAAAT
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GVLSNISSITDLGGFDPWHLFLAVGGVWFILGFAGCIGALFENITGLSVFLGIIFFLEL
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PQFEKWLQDNLTIVAGIFIGIALLQIFGICLAQNLVSDIEAVRASW"
354 c 384 g 345 t 16 others
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/db_xref="GI:2995865"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.linl.gov Series: IRAL Plate: 24 Row: k Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10440362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (09-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.systemsbiology.org
contact: amadan@systemsbiology.org
anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                       /product="Similar to RIKEN cDNA 2210021G21 gene"
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protein_id="AAH10405.1"
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HTKGCVGQFFKWLQDNLIVVAGVFMGIALLQIFGICLAQNLEQME"
a 662 c 716 g 541 t
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61. .852
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                                                                      CCTTCTCCTGCTGCGTCAGGGACCCTGCGGAGGATGTCCTCAACACCCAGTGTGGCTAC
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Search completed: December 19, 2002, 07:10:36 Job time: 2604 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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2183.116 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

11111 11111 111111 1111111111111111111	Result No.
1383 1383 1387.5 1287.5 1276.1 1276.1 1276.5 1244.5.5 1244.5.5 1223 1197.5 1117.3 1117.3 1117.3 1117.1 1117.3 1117.1 1118.8 1119.7 1117.3 1117.3 1117.1 1118.8 1119.7 1118.8 1119.7 1109.7 1109	0 44
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## ALIGNMENTS

REFERENCE AUTHORS TITLE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	BQ212057	RESULT 1
l (bases 1 to 899) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	human.	EST.	BQ212057.1 GI:20391921	BQ212057	5', mRNA sequence.	AGENCOURT_7594385 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6061320	BQ212057 899 bp mRNA linear EST 02-MAY-2002		

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                  AspTrpAspLeuAsnValTyrPheAsnCysSerGlyAlaSerTyrSerArgGluLysCys 180
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                                                                      CAAAACCTCATCGACTCCCTTCAGAAAGCTAACCAGTGCTGTGGCGCATATGGCCCTGAA
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC Clone distribution information can be
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/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pcMV-SPORT6; Si
/note="Organ: skin; Vector: pcMV-SPORT6; Si
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/clone="IMAGE:6061320"
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AGENCOURT_6625806 NIH_MGC_116
5', mRNA sequence.
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High quality sequence stop: 700.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLAM12803 row:
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                                                       218
                                                 /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORTS; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of stomachs, 62 yo male and 70 yo female. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetic tracking code 023. Note: this is a NIH_MCC Library."
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High quality sequence stop: 821.
Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver,
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/clone=lib="NCI_CGAP_Skn3"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: skin; Vector pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally primer: Oligo dT.
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Technologies. Note: this is a NCI_CGAP Library."
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1 (bases 1 to 1125)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
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Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
                                                                  /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORTG; Site_1: NotI; Site_2: ECORV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
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                                                                                                                                                             erAspIleGluAla-ValLysAlaGlyHisHisPhe
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                                                              GACCGGTTCCGGGAGTTCTTCGAGAGCAACATCAAGTCCTACCGGGACGATATCGATCTG
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: AFCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1759 row: d column: 03 High quality sequence stop: 786.
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National Institutes of Health, Mammalian
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/clone_lib="NIH_MGC_43"
/clone_lib="NIH_MGC_43"
/tlssue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: poTB7; Site_1: xhoI; Site_2:
ECORI, CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5;
adaptor: GGCACGAG(6). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MCC_Library. | "
Note: this is a NIH_MCC_Library. | "
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library." a 236 c 246 g 216 t
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/clone="IMAGE:5226856"
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/lab_host="DH10B"
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                                                                                                           ArgAsnIleTyrIleValAlaGlyValPhe-IleAla-IleSerLeuLeuGlnIlePheG
                                                                                                                                                 LysTrpAspGluSerIlePheThrLysGlyCysIleGlnAlaLeuGluSerTrpLeuPro
                                                                                                                                                                                                                             SerGlyAlaSerTyrSerArgGluLysCysGlyValProPheSerCysCysValProAsp
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                                                        GOATCTTCCTG
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                                                                                                                                                                              CCTGCGCAAAAAGTTGTGAACACACAGTGTGGATATGATGTCAGGATTCAGCTGAAGAGC
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                                                                                                CGGAACATTTACATTGTGGCTGGCGTCTTCAATCGCCAATCTCGCTGTTGCAGATATTTG
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        bp mRNA linear EST 16-OCT-2001 sapiens cDNA clone IMAGE:5212233 5',
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{\tt IlePhePheLeuGluLeuAlaValAlaValLeuAlaPheLeuPheGlnAspTrpValArg}
                                                            GTGGGGGCTCTGCGGGAGAATATCTGCTTGCTCAACTTTTTCTGTGGCACCATCGTGCTC
                                                                                                   ValGlyAlaLeuArgGluAsnIleCysLeuLeuAsnPhePheCysGlyThrIleValLeu
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BI905852.1
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: LLAM11532 row: n column: 10
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National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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1. (bases 1 to 836)
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/clone_lib="NMAGE_5212233"
/clone_lib="NMAGE_118"
/tissue_type="leukcoyte"
/lab_host="NDH108"
/note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV
/note="Continue"
/note="Continue"
/note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV
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/db_xref="taxon:9606"
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                                                                                                                                    Email: cgapbs r@mail.nih.gov

Tissue Procurement: Jeffrey Green M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11818 row: b column: 04
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603288609F1 NCI_CGAP_Mam6 Mus
                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg,
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EST.
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BI663945
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National Institutes of Health, Mammalian
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="TMAGE:5322531"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating di
/dev_stage="5 months"
                                                                                         /organism="Mus musculus"
                                                                                                                ocation/Qualifiers
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                                                                                                                                                                                                                                                         Ph.D.
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Sciurognathi; Muridae;
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               carcinoma"
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Murinae; Mus
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DEFINITION

BQ572112 742 bp mRNA UI-M-FDO-byd-n-13-0-UI.rl NIH\_BMAP\_FDO

Mus

musculus linear

cDNA clone

19-JUN-2002

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Alignment
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elleAlaIleSerLeuLeuGlnIlePheGlyIlePheLeuAlaArgThrLeuIleSer
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| CATTGCCATCTCACTGTGCAGATTTTTTGGCATCTTCCG-GGGAGGACCCTGATCTCG
                                                                                                                                                                 GlyValProPheSerCysCysValProAspProAlaGlnLysValValAsnThrGlnCys
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                                                                                                                GlyTyrAspValArgIleGlnLeuLysSerLysTrpAspGluSerIlePheThrLysGly
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                                                                                                    GGCTATGATGTCCGGATTCAGCTGAAGAGCAG-TGGGATGAGTTCATCTTTACAAAAGGA
                                                                                                                                                     GGGGTACCCTTCTCCTGCTGTGCCAGATCCTGCACAAAAAGTCGTGAACACACAGTGT
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               123
         SerTyrAsnIleIlePheTrpLeuAlaGlyValValPheLeuGlyValGlyLeuTrpAla
                                                                                              AGCTACAATATCGTCTTTTGGCTGGCTGGAGTTGTCTTCCTTGGAGTCGGGCTGTGGGCA
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BQ572112
BQ572112.1 GI:
EST.
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Tissue Procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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/Clone lib="NIH BMAP FOO"
/Clone lib="NIH BMAP FOO"
/tissue_type="whole brain"
/dev_stage="embryo 12.5 dpc"
/lab_host="DHIOB (TI phage resistant)"
/lab_host="DHIOB (TI phage resistant)"
/lab_host="DHIOB (TI phage resistant)"
/lab_host="DHIOB (TI phage resistant)"
/lab_host="DHIOB TI phage resistant)
Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA, synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is TGACAGAGCC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Instututes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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/clone="IMAGE:5716812"
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Unpublished (2001)
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segref@genoscope.cns.fr, V
Location/Qualifiers
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and
                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODB005YG02"
                                            /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
                                                                        /sex="male"
                                                                                      /clone_lib="LTI_NFL004_NBC2"
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braries and normalization
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clone CS0DB005YG02 5
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BG913227 79
602811894F1 NCI_CGAP_Brn67
5', mRNA sequence.
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EST.
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Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLAM10887 row: l column: 23
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Contact: Robert St
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National Institutes of Health, Mammalian
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/clone_lib="NCI_CGAP_Brn67"
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                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg,
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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/organism="Homo sapiens"
//db_xref="taxon:9606"
//clone="IMAGE:6338432"
//clone="IMAGE:6338432"
//clone="IMAGE:6338432"
//clone_lib="NHH_MGC_47"
//tlssue_type="neuroblastoma, cell line"
//lab_host="D10B (phage=resistant)"
//note="Organ: brain; Vector: poTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM1741 row: k column: 10 High quality sequence stop: 754. Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
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/lab_host="DH10B (phage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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National Institutes of Health, M
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                                                          /organism="Homo sapiens"
//db_xref="taxon:9606"
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//clone_lib="NHIMEC_49"
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//lab_Nost="DH10B (phage-resistant)"
//lab_Nost="DH10B (phage-resistant)"
//note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-df priming. Directionally cloned into ECORI,XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
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               ocation/Qualifiers
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G02842735F1 NCI_CGAP_Mam4 M mRNA sequence.
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AspArgPheArgGluPhePheGluSerAsnIleLysSerTyrArgAspAspIleAspLeu
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Contact: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen
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National Institutes of Health, Mammalian
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
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/tissue_type="tumor, gross tissue"
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/strain="NMRI"
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Search completed: December 19, 2002, 07:45:49 Job time : 2012 secs

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-YGAPPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1: /cgn2_6/ptodata/

2: /cgn2_6/ptodata/

3: /cgn2_6/ptodata/

4: /cgn2_6/ptodata/
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               TELEFAX:
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equence 13, App	•	equence 12, App	equence 12, App	equence 12, App	e 12, App	equence 12, App	e 120, Ap	e 14, App	17,	17, App	, App	17, App	: 17, App	в 17, App	e 12, App	e 273, Ap	16, App	16,	, App	16,	16,	e 16, App	Ψ	62,	Appl	e 111, Ap	e 111, Ap	: 111, Ap	: 111, Ap	e 111, Ap	111,	N

## ALIGNMENTS

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Patent No. SUCHATION:
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
APPLICANT: MOVEL HUMAN TRANSMEMBRANE 4 SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: U:
FILING DATE: Herewith
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                475 CTGCTGCTGCTGGTGTTCCTGCTGGAGGCCACCATCGCCATCCTCTTCTTCGCCTAC
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                                                                                                                                                                                                         ValTyrPheAsnCysSerGlyAlaSerTyrSerArgGluLysCysGlyValProPheSer
AAGGTGTGGCTTCAGGAGAACCTG---CTGGCTGTGGGCATCTTTGGGCTGTGCACGGCG
                          GluSerTrpLeuProArgAsnIleTyrIleValAlaGlyValPhe---IleAlaIleSer 244
                                                         CTGCACGCCCCCGGCACCTGG-
                                                                                                                                              CysCysValProAspProAlaGlnLysValValAsnThrGlnCysGlyTyrAspValArg
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Mismatches:
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APPLICANT: Testa, Jacqueline E.

APPLICANT: Quigley, James P.

APPLICANT: Quigley, James P.

APPLICANT: Seandel, Marco

TITLE OF INVENTION: MONOCLONAL ANTIBOIDES THAT RECOGNIZE ANTITILE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS

FILE REFERENCE: SUNY

CURRENT APPLICATION NUMBER: US/09/333,599

CURRENT FILING DATE: 1999-06-15

NUMBER OF SEQ ID NOS: 5

SOFTMARE: Patentin Ver. 2.0

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Query Match:
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; LOCATION: (57)..(815)
US-09-333-599-5
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US-09-333-599-5
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Patent No. 6245898
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                   AspLeuGlnAsnLeuIleAspSerLeuGlnLysAlaAsnGlnCysCysGlyAlaTyrGly 158
                                                                                                                                                                                                                                                                                             ValValLeuValLeuMetValGlyValValMetPheThrLeuGlyPheAlaGlyCysVal
GCTGTGACCAGCGCTGTGGACCAGCTGCAGCAGGAGTTCCACTGCTGTGGCAGCAACAAC
                                                                                               ArgPheArgGluPhePheGluSerAsnIle---LysSerTyrArgAsp-----AspIle
                                                                                                                                                               PhePheLeuGluLeuAlaValAlaValLeuAlaPheLeuPheGlnAspTrpValArgAsp
                                                                                                                                                                                                   GCCACCTTCAAGGAGCGTCGGAACCTGCTGCGCCCTGTACTTCATCCTGCTCCTCATCATC
                                                                                                                                                                                                                                 GlyAlaLeuArgGluAsnIleCysLeuLeuAsnPhePheCysGlyThrIleValLeuIle 101
                                                                                                                                                                                                                                                                                                                                                                  GluLysGly---ValLeuSerAspLeuThrLysValThrArgMetHisGlyIleAspPro
                                                                                                                                                                                                                                                                                                                                                                                                   AATTGCTGCTTCTGGCTGGCCTGGCCTGTCATGGCAGTGGGCATCTGGACGCTGGCC
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                                                                GAGCTCAAGGAGAACCTGAAGGACACCATGACCAAGCGCTACCACCAGCCGGCCCATGAG
                                                                                                                                 TTTCTGCTGGAGATCATCGCTGGTATCCTCGCCTACGCCTACTACCAGCAGCTGAACACG
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NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 870
TYPE: DNA
ORGANISM: Homo sapiens
US-09-333-599-1
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US-09-333-599-1
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Patent No. 6245898
GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Testa, Jacqueline E.
APPLICANT: Quigley, James P.
APPLICANT: Seandel, Marco
TITLE OF INVENTION: WONOCLONAL ANTIBOIDES THAT RECOGNIZE ANTIGENS
TITLE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS
FILE REFERENCE: SUNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                813 TAC 815
                                                                                             762 TTTGGCATGATCTTCACGTGCTGCCTG-----TACAGGAGTCTCAAGCTGGAGCAC
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                                 230 CTCAAGAGTGACTACATCAGCCTGCCTGGCCTCAGGCACCTAC-----CTGGCCACA 280
                                                                                                                                                              110 TTCAACGAGAAGAAGACAACATGTGGCACCGTTTGCCTCAAGTACCTGCTGTTTACCTAC
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62 ValValLeuValLeuMetValGlyValValMetPheThrLeuGlyPheAlaGlyCysVal 81
                                                             43 GluLysGly----ValLeuSerAspLeuThrLysValThrArgMetHisGlyIleAspPro 61
                                                                                                                                                                           6 TyrSerAsnAlaLysValSerCys-----TrpTyrLysTyrLeuLeuPheSerTyr 22 :::::: ||| :::|||
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	ATA: IIS/08/705	API		
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	OPERATING SYSTEM: MS-DOS	140	·• ·•	
	PE: 3.5	MEI	٠.	
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	STATE: NEW JERSEY	STA	٠.	
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ts	OF INVENTION: Expression Products	TITLE	٠.	
uences and	E OF INVENTION: Human Genes, Sequence	TITLE	٠. ٠	
Hongjin Ji,	`	APPL.		
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TACAGGAGTCTCAAGCTGGAGCAC 856	TTTGGCATGATCTTCACGTGCTGCCTG	806	В	
rAspIleGluAlaVal	heGlyIlePheLeuAlaArgThrLeuIleSerAs	249	Qy	
GGGGATCGGCATTGCCTGTGTGCAGGTC 805	ATCCAGGAGCACCTGAGGGTCATTGGGGGCTGTGGGGATCGGCATTGCC	746	DЬ	
LeuLeuGlnIl	euProAr ::	229	Qy	
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erTr	LysSerLysTrpAspGluSerIlePheThrLysGlyCysIleGlnAlaLeuGluS	209	Qy	
CAACATCTACAAGGTGGAG 71	GTGGCTCTTTGTGGACAGCGAGACCATGCCTCCAACATCTACAAGGTGGAG	665	DЬ	
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3CTCACAGGAG 622		581	Дъ	
snCysSerGlyAlaSerTyrSerArgGlu 178	ProGluAspTrpAspLeuAsnValTyrPheAsnCysSerGlyAlaSerTyrSerArgGlu	159	Qy	
AGGAGTTCCACTGCTGTGGCAGCAACAAC 580	GCTGTGACCAGCGCTGTGGACCAGCTGCAGCAGGA	521	DЪ	
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	AentonClaBentonTlaBenCortonClatveAl	139	Q V	
	GAGCTCAAGGAGAACCTGAAGGACACCATGACCAAGCGTACCACCAGCCGGCCATGAG	461	В	
LysSerTyrArgAspAspIle 138	gGluPhePheGluSerAsnIle	122	Qy	
CTACGCCTACTACCAGCAGCTGAACACG 460	TTTCTGCTGGAGATCATCGCTGGTATCCTCGCCTA	401	DЪ	
laPheLeuPheGlnAspTrpValArgAsp 121	PhePheLeuGluLeuAlaValAlaValLeuAlaPheLeuPheGlnAspTrpValArgAsp	102	Qy	
GCTGTACTTCATCCTGCTCCTCATCATC 400	GCCACCTTCAAGGAGCGTCGGAACCTGCTGCTGCTGCTCATCATCCTGCTCCTCATCATC	341	DЪ	
snPhePheCysGlyThrIleValLeuIle 101	GlyAlaLeuArgGluAsnIleCysLeuLeuAsnPhePheCysGlyThrIleValLeuIle	82	Qy	
rcanggrgacrédégrerredéériéerec 340	GTGGTGGCGGCACT	281	망	
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TELEFAX: 973-994-1/4,
TELEFAX: 973-994-1/4,
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1344 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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; MOLECULE TYPE:
US-08-705-771-8
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NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
TELEFAX: 973-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 nIleTyrIleValAlaGlyValPheIleAlaIleSerLeuLeuGlnIlePheGlyIlePh :::::: ||| :::|||| ||| |||
                                                                                                                                                           193 GlnLysValValAsnThrGlnCysGlyTyrAspVal-ArgIleGlnLeuLysSerLysTr 212
                                                                                                                                                                                                                  173 AlaSerTyrSerArgGluLysCysGlyValProPheSerCysCysValProAspProAla
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                                                                                     212 pAspGluSerIlePheThrLysGlyCysIleGlnAlaLeuGluSerTrpLeuProArgAs 232
                                                                                                                                                                                                                                                                                                                                                                                                                                           116 GlnAspTrpValArgAspArgPhe---ArgGluPhePheGluSerAsnIleLysSerTyr
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                                                    GTGGAGGGCCGTG----
                                                                                                                                                                                               -----AACGCCACGCGGTACCTGACTCCTGCTGCTTGGAG------
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70	ValLeuMetValGlyVal ::::::	pProValValLeuV	lyIleAspProV	54 ThrArgMetHisGlyIleAs	Qу
202		::: AACAACTTCGGAGTGCTC-	: TGCTGATCCAC <i>I</i>	1	
53		AlaTrpSerGluLysGlyValLeuSerAspLeuThrLysVal	AlaTrps	36 ValGlyLeuTrp-	Qy
35 160		LysTyrLeuLeuPheSerTyrAsnIleIlePheTrpLeuAlaGlyValValPheLeuGly       :::       :::    ::::      :::       AAGTATGTCCTGTTTTCTTCAACTTGCTCTTTTGGATCTGTGGCTGCATTTTGGGC	heSerTyrAsn]  -  :::   :  TTTTCTTCAACT	16 LysTyrLeuLeuP      ::::     101 AAGTATGTCCTGT	р бу
		7-044-4 (1-1452)	x US-08-807	905-674-2 (1-270)	US-09-
	1452 62 46 89 55	Length: Matches: Conservative: Mismatches: Indels: Gaps:	9.83e-23 259.50 42.86% 24.60% 17.91%	<pre>ent Scores: No.: t Similarity: coal Similarity: Match:</pre>	Alignment Pred. No.: Score: Percent S: Best Local Query Matc DB:
			ж н !	TOPOLOGY: linear MMEDIATE SOURCE: LIBRARY: GenBank CLONE: 180140 807-044-4	; ; ; ; ; ; ;
			se pairs cid	LENGTH: 1452 ba	
			ID NO: 4:	TELEX: ORMATION FOR SEQ EQUENCE CHARACTER	
			INFORMATION: 855-0555 5-4166	TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555 TELEFAX: 415-845-4166	
		9 F-0224 US	Lucy J. BER: 36,749 NUMBER: PR	NAME: Billings, REGISTRATION NUM.	
			ORMATION:	FILING DATE: TTORNEY/AGENT INF	
			530 DATA: ER:	CLASSIFICATION: RIOR APPLICATION   APPLICATION NUMB	
		807,044	ER: US/08/807,044 rewith	APPLICATION NUMB FILING DATE: He	
		ows Version 2.0	EQ for Windows N DATA:	SOFTWARE: FastS JRRENT APPLICATIO	
			skette ompatible : DOS	MEDIUM TYPE: D1 COMPUTER: IBM C OPERATING SYSTEM	
			FORM:	ZIP: 94304 OMPUTER READABLE	
				STATE: CA COUNTRY: USA	
			rter Drive	STREET: 3174 Po CITY: Palo Alto	
		uticals, Inc.	KESS: te Pharmaceuti	ADDRESSEE: Incy	
	SUPERFAMILY	HUMAN TRANSMEMBRANE 4	/EL	TILE OF INVENTION SECUENCE	
			nif K.	APPLICANT: Hillman, Jer APPLICANT: Goli, Surya	
		4		Patent No. 5863735 GENERAL INFORMATION:	
		744	on 115/08807044	)44-4	E S
	836	AGTGGTCAAGGCA	ATGTACTGGCAL	800 CTTCGCCATGACCATGTACTGGCAAGTG-	Db
	266	luA.	LeuIleSerAsp	252 eLeuAlaArgThr	Qy :
799		CTGCTGGCTGTGGGCATCTTTGGG-CTGTGCACGGCGCTGGTGCAGATCCTGGGCCTGAA	GCATCTTTGGG-	741 CTGCTGGCTGTGG	Db

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NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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5370 Manhattan Circle, Suite
                                                      Release #1.0, Version
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-905-674-2 (1-270) x PCT-US91-04986-1 (1-1452)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FRUGTH: 1452 base pairs
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NAME: Wall, Margaret M.
REGISTRATION NUMBER: 33,462
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APPLICATION NUMBER: US/07
FILING DATE: 13-JUL-1990
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NAME/KEY:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/379,076
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                                AsnGlnCysCysGlyAlaTyrGlyProGluAspTrpAspLeuAsnValTyrPheAsnCys 170
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CTGCAGTGTTGTGGTATAAATGGCACGAGTGATTGG-----
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                                                                      IleLysSerTyrArgAspAspIleAspLeuGlnAsnLeuIleAspSerLeuGlnLysAla
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PCT-US91-04986-1

Sequence 1, Application PC/TUS9104986 GENERAL INFORMATION:

Seed, Brian

APPLICANT:

Aruffo, Alejandro Camerini, David Allen, Janet

Lauffer, Leander

APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:

Stamenkovic, Ivan Stengelin, Siegfried Amiot, Martine Oquendo, Carmen Simmons, David L.

STATE: CITY: Boulder STREET: ADDRESSEE:

Colorado

COUNTRY:

USA

80303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PO

PCT/US91/04986

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                                     TELEPHONE: (617) 523-340
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN,
           SEQUENCE CHARACTERISTICS:
LENGTH: 687 base pairs
                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 12-APR-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                REFERENCE/DOCKET NUMBER: 41777
TELECOMMUNICATION INFORMATION: (617) 523-3400
                                                                                                                                      APPLICATION NUMBER: JP 022321-1992
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
PROTECTION NUMBER: ACCEPTAGE 1025
                                                                                                                                                                                                APPLICATION NUMBER: JP 085396-1991 FILING DATE: 17-APR-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865552
FILING DATE: 09-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: MONOCLONAL ANTIBODY, TITLE OF INVENTION: PRODUCTION THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KOYAMA, MASARU
APPLICANT: MIYAKE, MASAYUKI
APPLICANT: SENOO, MASAHARU
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CITY: BOSTON
STATE: MASSAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UZIP: 02109
                                                                                                                           REGISTRATION NUMBER:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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US-09-905-674-2 (1-270) x US-08-254-493-2 (1-687)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 LysTyrLeuLeuPheSerTyrAsnIleIlePheTrpLeuAlaGlyValValPheLeuGly
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Matches:
Conservative:
Mismatches:
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RESULT 8
US-08-408-222B-2
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                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                      US-08-408-222B-2
                              US-09-905-674-2 (1-270) x US-08-408-222B-2 (1-687)
                                                                                                                           Score
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                                                                                                                                                                                                    ORIGINAL SOURCE:
ORGANISM: huma
CELL TYPE: bre
CELL LINE: ZR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-085396-1991
FILING DATE: 14-APR-1991
PRIOR APPLICATION DATA:
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ADDRESSEE: Dike, Bronstein, Roberts & Cushman
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APPLICANT: Miyake, Masauyki
APPLICANT: Senoo, Masaharu
TITLE OF INVENTION: MONOCLO
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                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 687 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP-0 FILING DATE: 07-FEB-1994 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
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                                                                                                                                          No.:
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SOFTWARE: FastSEQ Version 1.5
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                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
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REFERENCE/DOCKET NUMBER: 41777-DIV
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 16 LysTyrLeuLeuPheSerTyrAsnIleIlePheTrpLeuAlaGlyValValPheLeuGly
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07-FEB-1994
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22-MAR-1995
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US-08-408-222B-3
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                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                        NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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STREET: τυς
STREET: Δυς
Boston
                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 CTGTTCTTCGGCTTCCTCTTGGTGATATTCGCCATTGAAATAGCTGCGGCCATCTGGGGA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 ATGCTGGTGGGCTTCCTGGGCTGCGGGGCTGTGCAGGAGTCCCAGTGCATGCTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 AATAATAATTCCAGCTTCTACACAGGAGTCTATATTCTGATCGGAGCCGGCGCCCTCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 ValThrArgMetHisGlyIleAspProValValLeuValLeuMetValGlyValValMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 ATTGGACTATGGCTCCGATTCGACTCTCAGACCAAGAGCATCTTCGAGCAAGAAACTAAT 150
                                                                         COUNTRY:
COMPUTER: IBM CO
OPERATING SYSTEM:
                                                               ZIP:
                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValGlyLeuTrpAlaTrpSerGlu------LysGlyValLeuSerAspLeuThrLys 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PhePheCysGlyThrIleValLeuIlePhePheLeuGluLeuAlaValAlaValLeuAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TrpAspGluSerIlePheThr---LysGlyCysIleGlnAlaLeuGluSerTrpLeuPro 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaGlnLysValValAsnThrGlnCysGlyTyrAspValArgIleGlnLeuLysSerLys 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----CAGTTTATCTCAGACATCTGC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnCysCysGlyAlaTyrGlyProGluAspTrpAspLeuAsnValTyrPheAsnCysSer 171
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                                                                                                                                                                                                                                                                                                                                                                       ATGATCTTCAGTATGATCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgAsnIleTyrIleValAlaGlyValPheIleAlaIleSerLeuLeuGlnIlePheGly
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                                                               02109
                                                                                                                            130 Water Street
                                                                                                                                                                                                                       Koyama, Masaru
Miyake, Masauy
                                                                              USA
                                                                                                                                                                                          Senoo, Masaharu
VENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES
                                                                                                                                                                                                                                                        Ikeyama,
                                                                                                                                         Dike, Bronstein, Roberts & Cushman
             IBM Compatible
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/254,493
FILING DATE: 06-7UN-1994
PRIOR APPLICATION DATA:
APPLICATION DATA: JP-079996-1991
FILING DATE: 12-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-085396-1991
FILING DATE: 14-APR-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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NAME/KEY: Coding Sequence
LOCATION: 112...795
OTHER INFORMATION: E Mat peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No . .
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ORIGINAL SOURCE:
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FILING DATE: 07-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,335
REGEDENATE JACANEM NUMBER: 41777-DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/408,
FILING DATE: 22-WAR-1995
CLASSIFICATION: 536
382 CTGTTCTTCGGCTTCCTCGTGATATTCGCCATTGAAATAGCTGCGGCCATCTGGGGA 441
                                                                                                                                           262 AATAATAATTCCAGCTTCTACACAGGAGTCTATATTCTGATCGGAGCCGGCGCCCTCATG 321
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                                                                                                                                                                                                                                                                                                             16 LysTyrLeuLeuPheSerTyrAsnIleIlePheTrpLeuAlaGlyValValPheLeuGly 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: human
CELL TYPE: breast carcinoma
CELL LINE: ZR-75-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                  PhePheCysGlyThrIleValLeuIlePhePheLeuGluLeuAlaValAlaValLeuAla 112
                                                                                                                                                                             ValThrArgMetHisGlyIleAspProvalValLeuValLeuMetValGlyValValMet 72
                                                                                                                                                                                                                  ATTGGACTATGGCTCCGATTCGACTCTCAGACCAAGAGCATCTTCGAGCAAGAAACTAAT 261
                                                                                                                                                                                                                                                                                        AAATACCTGCTGTTCGGATTTAACTTCATCTTCTGGCTTGCCGGGATTGCTGTCCTTGCC 201
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17.77%
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Matches:
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	TRANCEUNESS: SINGLE		
	YPE: nucleic		
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	TELEX: 421792		
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	INFORMATION:	; TE	
	REFERENCE/DOCKET NUMBER: 2026-4172		
	RICHARD W. BORK		
	ORNEY/AGENT INFO	; AT	
	FILING DATE: 28-APR-1995 CLASSIFICATION: 514		
	PPLICATION NUMBER: US		
	DATA:	; cu	
	OFTWARE:		
	TEM PC COMPATIBLE		
	PE: FLOR	• ••	
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	YORK	••	
	34		
	VDENCE ADDRESS:		
	OF SEQUENCES: 20	, NU	
*****	INVENTION: HUMAN METASTASIS SUPPRESSOR GENE KAI	; TI	
	OF INVENTION: CENE THERAPY ISTNO REAGENTS	 	
	Threwmron, Diamb, Patricia W.;	 AP	
	Dong, Jin-Tang; Barrett,	; AP	
	INFORMAT	Œ	
		<pre>; Sequence ; Patent N</pre>	
	30-225A-19	US-08-4	
	42 ATCATOTTCACTATCATCTTC 763	Dh 7	
	51 IlePheLeuAlaArgThrLeu 257	Qy 2	
ATTTGGC 74	ATCATCGGCGCAGTGGGCATCGGCATTGCCGTGGTCATGAT	Db 6	
heGly 25	31 ArgAsnIleTyrIleValAlaGlyValPheIleAlaIleSerLeuLeuGlnIl	Qy 2	
TCGAC 68	FIGAAGTCCTGTCCTGATGCCATCAA	Db 6	
euPro 23	212 TrpAspGluSerIlePheThrLysGlyCysIleGlnAlaLeuGluSerTrpLeuP 	Qy 2	
63	16 AAGAAGGACGT	Db 6	
erLys 21	92 ALAGINLYSVALVALASnThrGlnCysGlyTyrAspValArgIleGlnLeuLysS	7 40	
ccc 61	92CAGITTATCICAGACATCTGC		
3=	92CAGTUTATOTOAGACATOTOGO	Db 5	
spPro 19	.72 GlyAlaSerTyrSerArgGluLysCysGlyValProPheSerCysCysValProAs	Ωу 1	
59	62 AACTGCTGTGG	Db 5	
ysSer 17	52 GlnCysCysGlyAlaTyrGlyProGluA	0у 1	
CGTTG 56	02 AAGCTGAAAACCAAGGATGAGCCCCAGCGGGAAACGCTGAAAGCCA	Db 5	
AlaAsn 15	33 SerTyrArgAspAspIleAspLeuGlnAsnLeuIleAspSerLeuGlnLys	0у 1	
ACAAC 50	GGAGTTTTACA	Db 4	
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DB:
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                                                                Sequence 2, Application US/08855140 Patent No. 5854022
                                                    GENERAL INFORMATION:
     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.:
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                                                                                                                                                                   SerLeuLeuGlnIlePheGlyIlePheLeuAlaArgThrLeuIleSerAspIleGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGCTGTACTTTGCTTTCCTGCTCCTGATCCTCAFTGCCCAGGTGACGGCCGGGGCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATACTTTCTCTTCCTCTTCAACTTGATCTTCTTTATCCTGGGCGCAGTGATCCTGGGC
                                                                                                                                               GCCATCATCGAGCTCCTGGGGATGGTCCTGTCCATCTGCTTGTGCCGGCACGTCCATTCC
                                                                                                                                                                                                                                        AlaLeuGluSerTrpLeuProArgAsnIleTyrIleValAlaGlyValPheIleAlaIle 243
                                                                                                                                                                                                                                                                                                                                                                                                                                     AsnCysSerGlyAlaSerTyrSerArgGluLysCysGlyValProPheSerCysCysVal 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysAlaAsnGlnCysCysGlyAlaTyrGlyProGluAspTrpAspLeuAsnValTyrPhe ::::||| | | | | | | |
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                                                                                                                                                                                                                                                                          AGGACCCAGAGTGGCAACCACCCTGAGGACTGGCCTGTGTACCAGGAGGGCTGCATGGAG
                                                                                                                                                                                                                                                                                                      ArgIleGlnLeu---LysSerLysTrpAspGluSerIlePheThrLysGlyCysIleGln 223
                                                                                                                                                                                                                                                                                                                                        AAGGGGGAAGAGGACAACAGCCTTTCTGTGAGGAAGGGCTTCTGCGAGGCCCCCGGCAAC
                                                                                                                                                                                                                                                                                                                                                                      ProAspProAlaGlnLysValValAsnThrGlnCysGlyTyr-----AspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysSerTyr-----ArgAspAspIleAspLeuGlnAsnLeuIleAspSerLeuGln 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaPheLeuPheGlnAspTrpValArgAspArgPheArgGluPhePheGluSerAsnIle 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AsnPhePheCysGlyThrIleValLeuIlePhePheLeuGluLeuAlaValAlaValLeu 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCTCGCTTAGGATG - - - -
Hillman, Jennifer L.
Bandman, Olga
Goli, Surya K.
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Best Local Similarity:
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TOPOLOGY: LINC.

IMMEDIATE SOURCE:

LIBRARY: MYOMNO'

TONE: 779308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US FILING DATE: Herewith CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 977 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Guegler, TITLE OF INVENTION:
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                  113
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                                                                                                                                                                                                                                                                                                       140 TGCTGCTTGAAGTACATGATGTTCCTCTTCAATTTGATATTCTGGCTCTGTGGCTGTGGG
                                                                                                                                            73
                                                                                                                                                                                                                                                                   33 PheLeuGlyValGlyLeuTrpAlaTrpSerGluLysGlyValLeuSerAspLeuThrLys 52
                                                                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
             PheLeuPheGlnAspTrpValArgAspArgPheArgGluPhePheGluSerAsnIleLys
                                                                                                                                                                                                                                                                                                                    CysTrpTyrLysTyrLeuLeuPheSerTyrAsnIleIlePheTrpLeuAlaGlyValVal
                                             AGCTTTTTCATCGTCCTGGTCACCCTCCTAGCAGAGCTGATCTTACCCATCCTCTTC
                                                                                                                                                                            TCCCCCAGCTTCCCTTCGTTGTCTGCAGCCAACCTGGTCATCGCCATAGGCACCATTGTC
                                                                                                                                                                                                                                        CTGCTGGGAGTGGGCATCTGGCTCTCCGTGTCCCAAGGCAACTTTGCC-----ACCTTC
                                                                           PhePheCysGlyThrIleValLeuIlePhePheLeuGluLeuAlaValAlaValLeuAla 112
                                                                                                             ATGGTGACGGGCTTCCTCGGCTGCCTGGGGGCCATCAAGGAAAACAAGTGCCTCCTCCTC
                                                                                                                                PheThrLeuGlyPheAlaGlyCysValGlyAlaLeuArgGluAsnIleCysLeuLeuAsn
                                                                                                                                                                                                        ValThrArgMetHisGlyIleAspProValValLeuValLeuMetValGlyValValMet 72
94304
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NEW TRANSMEMBRANE
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Gaps:
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Matches:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 085396-1991
FILING DATE: 17-APR-1991
                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 07/865552
APPLICATION NUMBER: US 07/865552
FILING DATE: 09-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 079996-199
FILING DATE: 12-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MIYAKE, MASAYUKI
APPLICANT: SENOO, MASAHARU
TITLE OF INVENTION: MONOCLONAL ANTIBODY,
TITLE OF INVENTION: PRODUCTION THEREOF
                                REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 41777
TELECOMMUNICATION INFORMATION:
                                                                                                  APPLICATION NUMBER: JP 022321-1992
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 SerLysTrpAspGluSerIlePheThrLysGlyCysIleGlnAlaLeuGluSerTrpLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 SerGlyAlaSerTyrSerArgGluLysCysGlyValProPheSerCysCysValProAsp
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LENGTH: 1120 base pair
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212 TrpAspGluSerIlePheThr---LysGlyCysIleGlnAlaLeuGluSerTrpLeuPro 230
                                           616 AAGAAGGACGTACTCGAAACC-----
                                                                              192 AlaGlnLysValValAsnThrGlnCysGlyTyrAspValArgIleGlnLeuLysSerLys
                                                                                                                                                              172
                                                                                                                                                                                                     562
                                                                                                                                                                                                                                    152 GlnCysCysGlyAlaTyrGlyProGluAspTrpAspLeuAsnValTyrPheAsnCysSer 171
                                                                                                                                                                                                                                                                                                                       133
                                                                                                                                                                                                                                                                                                                                                              442 TATTCCCACAAGGATGAGTGTATTAAGGAAGTCCAGGAGTTTTACAAGGACACCTACAAC
                                                                                                                                                                                                                                                                                                                                                                                                   113 PheLeuPheGlnAspTrpValArgAspArgPheArgGluPhePheGluSerAsnIleLys 132
                                                                                                                                                                                                                                                                                                                                                                                                                                              382 CTGTTCTTCGGCTTCCTTGGTGATATTCGCCATTGAAATAGCTGCGGCCATCTGGGGA 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 ATGCTGGTGGGCTTCCTGGGCTGCTGCGGGGCTGTGCAGGAGTCCCAGTGCATGCTGGGA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 AATAATAATTCCAGCTTCTACACAGGAGTCTATATTCTGATCGGAGCCGGCGCCCTCATG
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                                                                                                                                                          GlyAlaSerTyrSerArgGluLysCysGlyValProPheSerCysCysValProAspPro
                                                                                                                                                                                                     AACTGCTGTGGTTTGGCTGGGGGCGTGGAA - - - - -
                                                                                                                                                                                                                                                                                    AAGCTGAAAACCAAGGATGAGCCCCAGCGGGAAACGCTGAAAGCCATCCACTATGCGTTG
                                                                                                                                                                                                                                                                                                                     SerTyrArg---AspAspIleAspLeuGlnAsnLeuIleAspSerLeuGlnLysAlaAsn 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PheThrLeuGlyPheAlaGlyCysValGlyAlaLeuArgGluAsnIleCysLeuLeuAsn
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Matches:
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716 GATGACAATAAGCACGTGCTT 736

230 ProArgAsnIleTyrIleVal 236

CTGGGGGAGAAC----

RESULT 12 US-08-254-493-3

Sequence 3, Application Patent No. 5439886

GENERAL INFORMATION:

APPLICANT:

KOYAMA, MASARU

IKEYAMA, SHUICHI

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:

ADDRESSEE:

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY: STREET: 130 | CITY: BOSTON

MASSACHUSETTS

02109

CLASSIFICATION: 435 FILING DATE:

APPLICATION NUMBER:

PRIOR APPLICATION DATA:

RESNICK, DAVID S.

(617) 523-6440

(617)

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                                                                US-09-905-674-2 (1-270) x US-08-808-148-2 (1-933)
                                                                                                         DB:
                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                   Query Match:
                                                                                                                                                                     Score:
                                                                                                                                                                                    Pred. No.:
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SEQUENCE CHARACTERISTICS:
LENGTH: 933 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION UNUBER: US/08/808,148
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMEER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REFERENCE/DOCKET NUMBER: PF-0218 US
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-845-4166
TELEPAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hillman, Jennifer
APPLICANT: Goli, Surya
APPLICANT: Zhang, Hong Wolfe
TITLE OF INVENTION: NOVEL HUMAN TUMOR-ASSOCIATED ANTIGEN
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                  TOPOLOGY: line
IMMEDIATE SOURCE:
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ADDRESSEE: Incyte PM
116 ACAGGAGCCACCATGCAGTGCTTCAGCTTCATTAAGACCATGATGATGCTCTTCAATTTG 175
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CITY: Palo Alto
STATE: CA
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CLONE: 2187263
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                            SerAsnAlaLysValSerCys-----TrpTyrLysTyrLeuLeuPheSerTyrAsnIle 24
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Matches:
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	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30	·· ··
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	LO I	•••
	STATE: WA	
	CITY: Seattle	<b>.</b>
	SEED and BERRY LLP	
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R AND METHODS	TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER NUMBER OF SECTIONS: 178	
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	820 TGTGTCCATGTATCTGTACTGCAATCTACAATAAGTCCACTTC 862	ਸ ਨ
	AlaArgThrLeulleSerAspIleGluAlaValLysAlaGlyHis	ξ.
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252	IlePh	Qy
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135		Qy
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354	295 GGGCTACTTCCTCATCGCAGCCGGCGTTGTGGTCTTTGCTCTTGGTTTTCCTGGGCTGCT	Db
81		Qy
294	235 GGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCATGCAGGTTGCAACGT	Db
61		Qy
234	-	DЬ
44	25 IlePheTrpLeuAlaGlyValValPheLeuGlyValGlyLeuTrpAlaTrpSerGluLys	Qy

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 1289 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/020,956

FILING DATE: 09-FEB-1998

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.4270

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 ACAGGAGCCACCATGCAGTGCTTCAGCTTCATTAAGACCATGATGATCCTCTTCAATTTG 170
                                                                                                                                                                                                                                                                      121 pargPheArgGluPhePheGluSerAsnIle------LysSerTyrAr 135
                                                                                                                                                                                                                                                                                                                 410 CTTCATTGCTGAGGTTGCAGCTGCTGGTGGTCGCCTTGGTGTAC-----AC 454
                                                                                                                                                                                                                                                                                                                                                                                       350 TGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCCTCCTCCTCAT 409
192 aGlnLysValValAsnThrGlnCysGlyTyrAspValArgIleGlnLeuLysSerLysTr 212
                                                                                                         575 CTTCACCAACTATACGGATTTTGAGGACTCACCCTACTTC-------
                                                                                                                                    155 yAlaTyrGlyProGluAspTrpAspLeuAsnValTyrPheAsnCysSerGlyAlaSerTy 175
                                                                                                                                                                           515 TTCCCAGGAAGACTTCACTCAAGTGTGGAACACCACCATGAAAGGGCTCAAGTGCTGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                           81 lGlyAlaLeuArgGluAsnIleCysLeuLeuAsnPhePheCysGlyThrIleValLeuIl 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerAsnAlaLysValSerCys-----TrpTyrLysTyrLeuLeuPheSerTyrAsnIle 24
                                                                                                                                                                                                                                                CTCATCTTTCTGTGGTGCAGCCCTGTTGGCAGTGGGCATCTGGGTGTC-AATCGATGG 229
                                                             rSerArgGluLysCysGlyValProPheSerCysCys------ValProAspProAl 192
                                    ----AAAGAGAACAGTGCCTTTCCCCCCATTCTGTTGCAATGACAACGTCACCAACACAGC
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US-09	Alignment Pred. No. Score: Percent S Best Loca Query Mat DB:	US-09-		RESULT 15 US-09-030-6 Sequence Patent No GENERAL APPLIC APPLIC APPLIC CORRES NUMBES CORRES ADDIC STRIC	Qу	Qу Дъ	ОУ	Db
-905-674-2 (1-270) x US-09-030-607-111 (1-1289) 7 SeråsnålaLysValSerCysTrpTyrLysTyrLeuLeuPheSerTyrÅsnīle 24	Alignment Scores: 1.12e-17 Length: 1289 Pred. No.: 218.50 Matches: 72 Score: 218.50 Matches: 72 Percent Similarity: 44.098 Conservative: 51 Best Local Similarity: 25.818 Mismatches: 112 Query Match: 15.088 Gaps: 8  DB:	NAME: Maki, David J.  REGISTRATION NUMBER: 31,392 REFERENCE/DOCKET NUMBER: 210121.427C3 REFERENCE/DOCKET NUMBER: 210121.427C3 TELECOMMUTICATION INFORMATION: TELEPHONE: (206) 622-4900 TELEPAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 111: SEQUENCE CHARACTERISTICS: LENGTH: 1289 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CNA ORGINALSOURCE: CNA ORGINALSOURCE: CNA ORGANISM: Homo sapiens	STATE: WA COUNTRY: USA ZIP: 98104 OMPUTER READAB MEDIUM TYPE: COMPUTER: IB OPERATING SYS SOCTWARE: PA URRENT APPLICA APPLICATION FILING DATE: CLASSIFICATIO	111, 111, 5. 62 1 NFC 1ANT: CA	252 eLeuAlaArgThrLeuIleSerAspIleGluAlaValLysAlaGlyHisHisPhe 270 ::::::	232 nIleTyrIleValAlaGlyValPheIleAlaIleSerLeuLeuGlnIlePheGlyIlePh 252	212 paspGluSerIlePheThrLysGlyCysIleGlnAlaLeuGluSerTrpLeuProArgAs 232 717	671 CAATGAAACCTGCACCAAGCAAAAAGGCTCACGACCAAAAAGTAGAG 716

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815 TGTGTCCATGTATCTGTACTGCAATCTACAATAAGTC-----CACTTC 857
                          252 eLeuAlaArgThrLeuIleSerAspIleGluAlaValLysAlaGlyHisHisPhe 270
                                                      232 nIleTyrIleValAlaGlyValPheIleAlaIleSerLeuLeuGlnIlePheGlyIlePh 252
                                                                                                                                                                   671 CAATGAAACCTGCACCAAGCAAAAGGCTCACGACCAAAAAGTAGAG----- 716
                                                                                                                                                                                                                          615 ----AAAGAGAACAGTGCCTTTCCCCCCATTCTGTTGCAATGACAACGTCACCAACACAGC
                                                                                                                                                                                                                                                  175 rSerArgGluLysCysGlyValProPheSerCysCys-----ValProAspProAl 192
                                                                                                                                                                                                                                                                               212 pAspGluSerIlePheThrLysGlyCysIleGlnAlaLeuGluSerTrpLeuProArgAs 232
                                                                                                                                                                                                                                                                                              155 yAlaTyrGlyProGluAspTrpAspLeuAsnValTyrPheAsnCysSerGlyAlaSerTy 175
                                                                                                                                                                                                                                                                                                                                   515 TTCCCAGGAAGACTTCACTCAAGTGTGGAACACCACCATGAAAGGGGCTCAAGTGCTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 GlyValLeuSerAsp-----LeuThrLysVal-ThrArgMetHisGlyIleAspPr 61
                                                                                                           -----GGTTGCTTCAATCAGCTTTGTATGACATCCGAACTAA
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                                                                                                                                                                                                                                                                                                                                     574
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Search completed: December 19, 2002, 07:46:59 Job time: 56 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2002, 01:02:16; Search time 260 Seconds (without alignments)
12022.206 Million cell updates/sec

Title: Perfect score: US-09-905-674-1 1388 1 cttcctcggccgag

Sequence: cttcctcggccgagccgggc.....gggaggcgngacgttggccc 1388

Scoring table:

2185239 seqs, 1125999159 residues IDENTITY\_NUC
Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database N\_Geneseq\_101002:\*

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## SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

RESULT 1 AAD29623 AAD29623 standard; cDNA; 1388 ВP

17-MAY-2002 (first entry) AAD29623;

Human tetraspan protein, TSPAN-7 encoding cDNA.

Human; tetraspan protein; TSPAN-7; hyperproliferative disorder; neoplastic disease; prostate cancer; antisense therapy; tumour; ss.

Homo sapiens.

Location/Qualifiers 67..879

/\*tag= a /product= "Human TSPAN-7 protein" 1234..1237

misc\_feature /\*tag=

/note= "These bases are given as YTY in the sequence shown as SEQ ID NO:1 in Fig 2 of the specification"

W0200206340-A2.

13-JUL-2001; 2001WO-US22134

24-JAN-2002.

14-JUL-2000; 2000US-218280P

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Matches 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to inhibitors of tetraspan protein, TSPAN-7 which are used to reduce or decrease the expression of TSPAN-7 in a mammalian cell and for treating hyperproliferative disorder, especially cancer in a mammal. The invention also provides TSPAN-7 polypeptides and polynucleotides. TSPAN-7 inhibitors are useful for inhibiting proliferation of mammalian cells, including tumour cells, for decreasing the side effects of cancer therapy and for treating neoplastic diseases. They are used to modulate TSPAN-7 expression and function in cancer cells, particularly in prostate cancer cells. They are also used in antisense therapy. The present sequence is human TSPAN-7 protein encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New inhibitor of tetraspan protein useful for reducing the expression or activities of tetraspan protein in cells, and for treating a hyperproliferative disorder, especially cancer in a mammal .
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1388; Conserv
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)B; AAE18535.
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 AAGTGCGGGGTCCCCTTCTCCTGCTGCGTGCCAGATCCTGCGCAAAAAGTTGTGAACACA
                                                                               GATCTGCAAAACCTCATCGACTCCCTTCAGAAAGCTAACCAGTGCTGTGGCGCATATGGC
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0; Mismatches
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                                  TTTGGGTCATCACATCTGTGGGTNGGCCGTGGGTAGAGGGACCCACAGGCGTGGACAGG
                                                                                                        ACTCTGAAAGACAGAGAGGGCTCCTGTGGCTGCCAGGAGGCCTTGACTCAGACCCCCTGC
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AAA93623 standard; DNA; 1428 ВP

AAA93623; 16-JAN-2001 (first entry)

tetraspanin-like protein splice variant SECX 3911675

ARASJACZ AAASJACZ AC AAAS XX AAAS XX AAAS XX Hume DT 16---XX Hume XX Hume XX Immu KW SEC) KW Immu KW infe KW skir KW skir KW skir KW skir SECX protein; human; secreted; membrane-associated; cancer; proliferation regulator; differentiation regulator; non-malignant tum proliferation regulator; differentiation regulator; non-malignant tum immune disorder; autoimmune disease; transplant rejection; allergy; A infection; inflammatory disorder; arthritis; haematopoietic disorder; skin disorder; cardiovascular disorder; atherosclerosis; restenosis; neurological disease; Alzheimer's disease; trauma; wounding; spinal cord injury; skeletal disorder; cytostatic; immunosuppressive; anti-HIV; antinflammatory; anti-hritinnon-malignant tumour; ection; allergy; AIDS;

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                                                                                                                                                                                                                                                                                  Sequences AAA93616-A93631 and AAA93675 represent nucleic acids which encode human SECX proteins (AAB23029-B23048). The SECX proteins CC of the invention are either secreted or membrane-associated proteins CC and act as regulator of cellular proliferation and differentiation. SECX proteins or nucleotides are useful for diagnosing the presence of, or CC proteins and nucleotides. The SECX proteins are also useful to screen CC compounds that modulate SECX activity or expression. The interaction of CC a SECX protein with other cellular proteins may be useful to modulate CC differentiation and cell survival. SECX nucleotides are useful for the CC recombinant expression of SECX protein, and may be useful to modulate CC excides equences are also useful for the CC acid sequences are also useful for the CC secX expression (e.g., using antisense oligonucleotides). SECX nucleic cuseful for detecting the presence of SECX nucleotides are useful for tissue type in CC useful for detecting the presence of SECX nucleotides and for screening CC tissue cultures for contamination. Diseases that may be treated or prevented using SECX proteins or nucleotides and for screening CC including autoimmune diseases, transplant rejection, allergies, AIDS), concluding autoimmune diseases, transplant rejection, allergies, AIDS), concurological diseases (e.g., Alzheimer's disease), trauma (e.g., catiosorders, cational concluding spinal conditions, and skeletal ccc disorders.
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Best Local Similarity 98.4
Conservative
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                                                                                                                                                                                                                                                                                Sequence 1428 BP;
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08-MAR-2000; 2000US-0123667.
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dermatological; gene therapy; ds.
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CAGAAGATGCACTATTATAGAGTACTCTAACGCCAAAGTCAGCTGCTGGTACAAGTACCTC 120
                                                                                                                                                     CTTTTCAGCTACAACATCATCTTCTGGTTGGCTGGAGTTGTCTTCCTTGGAGTCGGGCTG 180
                                                                     CAGAAGATGCACTATTATAGATACTCTAACGCCAAGGTCAGCTGCTGCTACAAGTACCTC
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                                                                                                                                                                                                                                                                            279 A; 408 C; 426 G; 315 T; 0 other;
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98.4%;
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; Pred. No. 0;
2; Mismatches
                                                                                                                                                                                                                                            DB 21; Length 1428;
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TGGGTAGAGGGACCCACAGGCGTGGACAGG 1320	1 TTTGGGTCATCCACATCTGTGGGTNGGCCGTGGGTAGAGG	126	Q
	0 AGCTCAAGCATGTCTGCAGGACACCCTGGT-CCCCTCTCC	123	В
CCCCTCTCCAYTGGCWTCCAGACATCTG	1 AGCTCAAGCATGTCTGCAGGACACCCTGGTCCCCCCTCTCC	120	ĮQ.
FGCCAGGAGGCTTGACTCAGACCCCCTGC 1229	0 ACTCTGAAAGACAGAGAGGGCTCCTGTGGCTGCCAGGAGG	117	마
TGCCAGGAGGGCTTGACTCAGACCCCCTG	1 ACTCTGAAAGACAGAGAGGGCTCCTGTGGCTGCCAGGAGG	114	γQ
CAGAGAATGTGTCTTTATGTGGGAGTGGTG 1140 	1 GACTGCATCCCTCTGGAGTCTACCCAGAGACAGAC	108	DP QA
CCCCCTTGATACCTGCCCAAACTTG	0 CTGTTTCTGCTTGCTGGTGCTGAAGACCAAGGGTC	105	DЬ
GGGTCCCCTTGTTACCTGCCCAAACTTGT 1080	1 CTGTTTCTGCTTGCTGCTGAAGACCAAGGGTC	102	Qy
CATCTTAAGCATCAGCGTGACGTGACCTC	0 GAGGAGCCGACACCCCAGAGCCAGTGCCCCATCTT	99	Дb
CATCTTAAGCATCAGCGTGACGTGAC	1 GAGGAGCCGACACCCCCAGAGCCAGTGCCCCCATCT	96	Qy
TCTCTGCCATCAGCCCTACGTCCAGAGGGA 989	0 AGCTGAGCCACGCTGGGAGGCCAGAGCCTTTCTC	93	da Ay
TTCTGAGGAGCAGAGTTGAGGGAGCCG 9	0 TCAGACATCGAGGCAGTGAAGACCGGCCATCA	87	) Db
TTCTGAGGAGCAGAGTTGAGGGAGCCG 90	1 TCAGACATCGAGGCAGTGAAGGCCGGCCATCA	. 84	γQ
TTTGCCATCTTCCTGGCAAGGACGCTGATC 869	O GICTICATCGCCATCTCGCTGTTGCAGATATT	81	Дb
TGGCATCTTCCTGGCAAGGACGCTG	1 GTCTTCATCGCCATCTCGCTGTTGCAGATATT	78	Qγ
CTCCCGCGAACATTTACATTGTGGCTGGC 809	0 AAAGGCTGCATCCAGGCGCTGGAAAGCTGGCTCC	75	ДĎ
CCCCGAACATTTACATTGTGGCTGG	1 AAAGGCTGCATCCAGGCGCTGGAAAGCTGGCTCC	. 72	γQ
AAGAGCAAGTGGGATGAGTCCATCTTCACG 720	1 CAGTGTGGATATGATGTCAGGATTCAGCTGAAG	69	Db Qy
CCAGATCCTGCGCAAAAAGTTGTGAACACA 689	O AAGTGCGGGGTCCCCTTCTCCTGCTGCGTGCCAGATCCTG	63	Дb
GATCCTGCGCAAAAAGTTGTGAACAC	1 AAGTGCGGGGTCCCCTTCTCCTGCTGCGTGCCAGATCCTG	60	Qγ
AATTGCAGCGGTGCCAGCTACAGCCGAGAG 629	0 CCTGAAGACTGGGACCTCAACGTCTACTTCAATTGCAGC	57	В
GCAGCGGTGCCAGCTACAGCCGAG	1 CCTGAAGACTGGGACCTCAACGTCTACTTCAATTGCAGG	54	Qy
AAAGCTAACCAGTGCTGTGGCGCATATGGC 569		51	ДD
GCTGTGGCGCATATGG	1 GATCTGCAAAACCTCATCGACTC	48	Qy
AGCAACATCAAGTCCTACCGGGACGATATC 5		45	ДĎ
agcaacatcaagtcctaccgggacgat	1 GTGAGGGACCGGTTCCGGGAGTTCTTCGAGAGCAACATC	42	Qγ
GCCGTGCTGCCTTCCTGTTCCAGGACTGG 449	0 GTGCTCATCTTCCTTGGAGCTGGCTGTGGCCGTGCT	39	Db
GCCGTGCTGGCCTTCCTGTTCCAGGACTG	1 GTGCTCATCTTCCTGGAGCTGGCTGTGGCCGTGCT	36	Qy
TGCTTGCTCAACTTTTCTGTGGCACCATC 389	0 GGCCGCGTGGGGGCGCGCAGGGAGATATCTGCTTGCTC	33	Дb
GCTTGCTCAACTTTTTCTGTGGCACCATC 3	1 GGCTGCGTGGGGGGCTCTGCGGGAGAATATCTG	30	Qy
GGCGTGGTGATGTTCACCCTGGGGTTCGCC 300	1 ATCGACCCTGTGGTGCTGGTCCTGATGGTGGG	24 27	Qy db
GACCTCACCAAAGTGACCCGGATGCATGG	0 TGGGCATGGAGCGAAAAGGGTGTGCTGTCCGACCTCAC	21	Дb
GACCTCACCAAAGTGACCCGGATGCATGGA 24	1 TGGGCATGGAGCGAAAAGGGTGTGCTGTCCGACCTCACC	18	, Qy

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RESULT 3
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13 - MAY - 1998;
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15 - MAY - 1998;
16 - MAY - 1998;
17 - MAY - 1998;
18 - MAY - 1998;
ANZ65250 to ANZ65350 represent 97 isolated human secreted protein genes. This sequence was found to be present on human chromosome 10.

ANX76124 to ANX76223 represent the secreted proteins encoded by the 97 human genes. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 97 genes, based on which tissues they are most highly expressed in, and include developing products for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autolamune disease; ellergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AIDS; leukaemia; therapy; chromosome 10; ds.
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                                                                                                                                                                                                                                           New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders -
                                                                                                                                                                                                                                                                                                                                                                                Lafleur
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Shi Y, Young
V, Endress GA,
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Wei F, Brewer LA,
ner R;
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Soppet DR;
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diagnosis or treatment of cancer, tumours, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney disorders, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. The sequences shown in AAY76224 to AAY76424 represent fragments of the
                                                                                                                                                                               CCTTCTCCTGCTGCGTGCCAGATCCTGCGCAAAAAGTTGTGAACACACAGTGTGGGATATG
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                                                   TCTCGCTGTTGCAGATATTTGGCATCTTCCTGGCAAGGACGCTGATCTCAGACATCGAGG
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CAGTGAAGGCCGGCCATCACTTCTGAGGAGCCAGAGTTGAGGGAGCCGAGCTGAGCCACGC
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                                              for the prevention, diagnosis disorders -
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  Claim 2;
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                                                                                                                                     2001-138647/14.
DB; AAB87034, AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGCAGGACACCCTGGTCCCCCTCTCCAYTGGCWTCCAGACATCTGCTTTGGGTCATCCA 1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGTGCTGAAGACCAAGGGTCCCCCTTGTTACCTGCCCAAACTTGTGACTGCATCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATCTGTGGGTGGGCCGTGGGTAGAGGGGACCCACAGGCGTGGACAGGGCATCTCTCCA 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCAGGACACCCTGGT; CCCCTCTCCACTGGCATCCAGACATCTGCTTTGGGTCATCCA
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332pp;
                                                            secreted TANGO and MANGO polypeptides, useful agnosis and treatment of, e.g. cancers and imm
                                                                                                                                                                                                                                  Kirst
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Query Match
Best Local Similarity
Matches 1317; Conserv

Conservative

2;

93.18; 99.28;

Score 1292.2;
Pred. No. 0;
2; Mismatches

DB 6;

22; Length Indels

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Gaps

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CC The invention relates to novel secreted/transmembrane proteins, and CC nucleic acids encoding them. The novel proteins are designated TANGO 339, CC TANGO 353, TANGO 358, TANGO 365, TANGO 368, TANGO 369, TANGO 383, TANGO CC 393, TANGO 402, MANGO 346 and MANGO 349 and are of human origin, and a CC murine TANGO 393 is also included within the scope of the invention. The CC invention also encompasses fragments and variants of the proteins of the invention and nucleic acids encoding them. The invention additionally CC relates to host cells comprising a nucleic acid of the invention; methods (CC for the production of a protein of the invention; and nutleous specific CC for a protein of the invention; and methods for detecting a protein or CC nucleic acid of the invention; and methods of identifying agents which CC bind to or modulate the activity of a protein of the invention. The novel CC secreted proteins, nucleic acids encoding them, and antibodies against them may be used in the prevention, diagnosis and treatment of diseases CC associated with inappropriate expression or activity of the secreted proteins. The secreted proteins. The secreted to compression or activity, which may be useful in CC invention e.g., cancers and immunological disorders. The present CC invention e.g., cancers and immunological disorders. The present CC sequence represents CDNA encoding human TANGO protein of the invention.
Sequence 2715 BP; 559 A; 760 C; 715 G; 681 T; 0 other;
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              GTTGTGAACACACAGTGTGGATATGATGTCAGGATTCAGCTGAAGAGCAAGTGGGATGAG
                                                          GGCGCATATGGCCCTGAAGACTGGGACCTCAACGTCTACTTCAATTGCAGCGGTGCCAGC
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                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #27820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS92016 standard;
  (HYSE-) HYSEQ
                                             31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                               WO200175067-A2
                                                                                                                                                                                                                                            Homo
                                                                                                            30-MAR-2001; 2001WO-US08631
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upplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                             2000US-0540217
2000US-0649167
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WPI; 200
                           Drmanac RT,
                           Liu
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                           Tang
                            YT
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

Claim 1; SEQ ID No 27820; 103pp; English

The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polypucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC specification, but was obtained in electronic format directly from WIPO case for the polypholyphical acts of this patent did not appear in the printed CC appetition of the coloring sequences of the invention. ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 2623 BP; 515 A; 713 C; 719 G; 659 T; 17 other;

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Query Match Best Local S

Local Similarity

91.9%;

Score 1275.4; Mismatches No. 0;

DB 23; 40;

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12 - MAY - 1998

13 - MAY - 1998

14 - MAY - 1998

18 - MAY - 1998
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Ruben SM, Olsen HS, P-PSDB; 2000-062296/05 DB; AAY76266. DW, Florence K, Shi Y, You Endress e K, Ni J, Rosen Young PE, Wei F, ss GA, Ebner R; ĽΑ, Soppet Moore pet DR;

New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders -

Disclosure; Page 427-428; 475pp; English.

CC AAX65250 to AAX65350 represent 97 isolated human secreted protein genes.

CC This sequence was found to be present on human chromosome 10.

CC AAY76124 to AAAY76223 represent the secreted proteins encoded by the 97

CC human genes. The genes and their corresponding secreted polypeptides are

CC useful for preventing, treating or ameliorating medical conditions,

CC e.g. by protein or gene therapy. Also pathological conditions can be

CC diagnosed by determining the amount of the new polypeptides in a sample

CC uses are described for each of the 97 genes, based on which tissues they

CC uses are described for each of the 97 genes, based on which tissues they

CC are most highly expressed in, and include developing products for the

CC diagnosis or treatment of cancer, tumours, developmental abnormalities

CC and foetal deficiencies, blood disorders, diseases of the immune system,

CC autolimune diseases, inflammation, allergies, Alzheimer's and cognitive

CC disorders, atherosclarosis, diabetes, cardiovascular disorders, kidney

CC disorders, digestive/endocrine disorders, infections and AIDS. The

CC olypeptides are also useful for identifying their binding partners.

CC The sequences shown in AAY76224 to AAY76424 represent fragments of the proteins

Sequence 323 Α, 469 <u>ن</u> 488 G; 387 Τ; 0

Query Match Best Local Sim Matches 1309; Local Similarity Conservative 85.7%; 95.8%; Score 1189.6; Pred. No. 3e-3 No. 3e-303 DB 21; Length 16; Gaps 8;

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27-APR-1999;
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22-DEC-1998;
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Secretory proteins play important roles in the proliferation control, differentiation induction, the material transport and the biophylaxis cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is the coding sequence for a human protein which has at least one hydrophobic domain. The protein encoded by the present sequence may be a secretory or a membra

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Best Local S
Matches 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein. The encoded protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopoiesis activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemacostatic and thrombolytic activity, anti-inflammatory activity and tumour inhibition activity. The present sequence could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's disease, and cancer via gene therapy.
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                                                                                               CAGTGTGGATATGATGTCAGGATTCAGCTGAAGAGCAAGTGGGATGAGTCCATCTTCACG
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                                    GTCTTCATCGCCATCTCGCTGTTGCAGATATTTGGCATCTTCCTGGCAAGGACGCTGATC
                                                                                   AAGTGCGGGGTCCCCTTCTCCTGCTGCGTGCCAGATCCTGCGCAAAAAGTTGTGAACACA
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Claim 2;

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English

disorders

Nucleic acids encoding secreted TANGO and MANGO polypeptides, for the prevention, diagnosis and treatment of, e.g. cancers  $\hat{\epsilon}$ 

and

immune

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CC The invention relates to novel secreted/transmembrane proteins, and Cnucleic acids encoding them. The novel proteins are designated TANGO 339, CC TANGO 353, TANGO 358, TANGO 365, TANGO 368, TANGO 369, TANGO 383, TANGO CC 393, TANGO 402, MANGO 346 and MANGO 349 and are of human origin, and a CC murine TANGO 393 is also included within the scope of the invention. The Ci invention also encompasses fragments and variants of the proteins of the invention and nucleic acids encoding them. The invention additionally CC relates to host cells comprising a nucleic acid of the invention; methods CC for the production of a protein of the invention; and artibody specific CC for a protein of the invention; and tetecting a protein of CC ucleic acid of the invention; and methods for detecting a protein of the invention; and methods of identifying agents which CC bind to or modulate the activity of a protein of the invention. The novel CC secreted proteins, nucleic acids encoding them, and antibodies against the may be used in the prevention, diagnosis and treatment of diseases CC associated with inappropriate expression or activity of the secreted CC proteins. The secreted proteins of expression or activity, which may be useful in CC invention e.g., cancers and immunological disorders. The present CC sequence represents CDNA encoding human TANGO protein of the invention.
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                                                                                                    CC The invention relates to novel secreted/transmembrane proteins, and CC nucleic acids encoding them. The novel proteins are designated TANGO 339, CC TANGO 353, TANGO 355, TANGO 365, TANGO 368, TANGO 383, TANGO 383, TANGO 37, TANGO 368, TANGO 368, TANGO 383, TANGO 383, TANGO 383, TANGO 383, TANGO 368, TANGO 368, TANGO 383, TANGO 383, TANGO 383, TANGO 383, TANGO 384, TANGO 384, TANGO 385, TANGO 384, TANGO 384, TANGO 385, TANGO 385, TANGO 384, TANGO 385, TANGO 385, TANGO 384, TANGO 385, TANGO 384, TANGO 385, TANGO 385, TANGO 384, TANGO 385, TANGO 385, TANGO 386, TANGO 384, TANGO 385, TANGO 386, TANGO 385, TANGO 386, TANGO 385, TANGO 386, TANGO 387, TANGO 386, TANGO 386, TANGO 386, TANGO 387, TANGO 386, TANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secreted protein; transmembrane protein; TANGO; human; drug screening; activity modulator; expression modulator; cancer; immunological disorder; cytostatic; immunomodulatory; gene therapy; ss.
                                    the treatment of disorders associated with the proteins of the invention e.g., cancers and immunological disorders. The present sequence represents cDNA encoding human TANGO protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding secreted TANGO and MANGO polypeptides, useful for the prevention, diagnosis and treatment of, e.g. cancers and immu
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Matches
Secreted protein; transmembrane protein; TANGO; human; drug screening; activity modulator; expression modulator; cancer; immunological disorder; cytostatic; immunomodulatory; gene therapy; ss.
                                          Human
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                                                                                                     AAF90657 standard; cDNA;
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les 811; Conservative
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                                                                                                                                                                           ATCGAGGCAGTGAAGGCCGGCCATCACTTCTGA 879
                                         variant cDNA ORF,
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The invention relates to novel secreted/transmembrane proteins, and convolute acids encoding them. The novel proteins are designated TANGO 339, CC TANGO 353, TANGO 358, TANGO 365, TANGO 368, TANGO 369, TANGO 383, TANGO CC 393, TANGO 402, MANGO 346 and MANGO 349 and are of human origin, and a cmarine TANGO 393 is also included within the scope of the invention. The cinvention also encompasses fragments and variants of the invention and nucleic acids encoding them. The invention additionally correlates to host cells comprising a nucleic acid of the invention; methods for the protein of the invention; methods for detecting a protein or convolute the activity of a protein of the invention; and antibody specific corrected proteins, nucleic acids encoding them, and antibodies against them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression or activity of the secreted corrected proteins of the invention may also be used to identify modulators of expression or activity, which may be useful in the treatment of disorders associated with the preventions of the invention of the invention of identify modulators of expression or activity of the secreted corrections. The secreted proteins of the invention may also be used to identify modulators of expression or activity, which may be useful in the treatment of disorders and immunological disorders. The present corrections of the invention of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser Pan Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding secreted TANGO and MANGO polypeptides, for the prevention, diagnosis and treatment of, e.g. cancers \epsilon disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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  Sequence 813
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DB; AAB87135.
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BP; 164 A; 213
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ATGCACTATTATAGATACTCTAACGCCAAAGTCAGCTGCTGGTACCAAGTACCTCCTTTTC 126
                                                                                                                                                      AGCTACAACATCATCTTCTGGTTGGCTGGAGTTGTCTTCCTTGGAGTCGGGCTGTGGGCA 186
                                                                                                                                                                                       ATGCACTATTATAGATACTCTAACGCCAAGGTCAGCTGCTGGTACAAGTACCTCCTTTAC
                                                CCTGTGGTGCTGGTCCTGATGGTGGGCGTGGTGATGTTCACCCTGGGGTTCGCCGGCTGC
                                                          CCTGTGGTGCTGGTCCTGATGGTGGTGGTGGTGATGTTCACCCTGGGGTTCGCCGGCTGC
                                                                                                                                          AGCTACAACATCATCTTCTGGTTGGCTGGAGTTGTCTTCCTTGGAGTCGGGCTGTGGGCA
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nilarity 99.8%;
Conservative
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Local Similarity

DB 22;

Length

813;

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367

ATCTTCTTCCTGGAGCTGGCTGTGGCCGTGCCTTCCTGTTCCAGGACTGGGTGAGG

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                                  Nucleic acids encoding for the prevention, dia disorders -
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   Claim
                                                                                                                                                                                                                                                                                         31-JUL-2000; 2000WO-US20935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human TANGO 339 A40V variant cDNA ORF,
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DB; AAB87136.
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282; 332pp;
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                                                   ing secreted TANGO and MANGO polypeptides, useful diagnosis and treatment of, e.g. cancers and imm
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Best Local S
Matches 811
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The invention relates to novel secreted/transmembrane proteins, and convoleic acids encoding them. The novel proteins are designated TANGO 339, CC TANGO 353, TANGO 365, TANGO 368, TANGO 383, TANGO 283, TANGO 383, TANGO CC 393, TANGO 402, MANGO 346 and MANGO 349 and are of human origin, and a company of the invention. The invention also encompasses fragments and variants of the proteins of the invention; and nucleic acids encoding them. The invention additionally convention, and nucleic acids encoding them. The invention additionally convention, and nucleic acids encoding them another protein of the invention; an antibody specific for the production of a protein of the invention; an antibody specific convention acid of the invention; and methods for detecting a protein or convention acid of the invention; and methods of identifying agents which convention acid to or modulate the acid encoding them, and antibodies against convention. The novel convention is the invention of the invention of associated with inappropriate expression or activity of the secreted convention. The novel consistency is the invention may also be used to consist the invention of activity of the secreted proteins. The secreted proteins of expression or activity, which may be used to consist the invention of activity of the secreted proteins.
Sequence 813 BP; 163 A; 212 C; 235 G; 203 T; 0 other;
                                                                                                                                     the treatment of disorders associated with the proteins of the invention e.g., cancers and immunological disorders. The present sequence represents cDNA encoding human TANGO protein of the invention.
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Local Similarity

811;

Conservative

0;

58.3%;

Score 809.8; I Pred. No. 2.7e.

.7e-203; BB 22;

Indels Length

Gaps

0;

813; 0,

727 601 541 607 481 547 421 487 361 427 301 367 241 307 181 247 121 187 127 61 67 ۲ CAAAACCTCATCGACTCCCTTCAGAAAGCTAACCAGTGCTGTGGCGCATATGGCCCTGAA GGATATGATGTCAGGATTCAGCTGAAGAGCAAGTGGGATGAGTCCATCTTCACGAAAGGC GGGGTCCCCTTCTCCTGCGGGGTGCCAGATCCTGCGCAAAAAGTTGTGAACACACAGTGT GACCGGTTCCGGGAGTTCTTCGAGAGCAACATCAAGTCCTACCGGGACGATATCGATCTG GACCGGTTCCGGGAGTTCTTCGAGAGCAACATCAAGTCCTACCGGGACGATATCGATCTG ATCTTCTTCCTGGAGCTGGCTGTGGCCGTGCTGCCTTCCTGTTCCAGGACTGGGTGAGG ATCTTCTTCCTGGAGCTGGCTGTGGCCGTGCTGGCCTTCCTGTTCCAGGACTGGGTGAGG GTGGGGGCTCTGCGGGAGAATATCTGCTTGCTCAACTTTTTCTGTGGCACCATCGTGCTC CCTGTGGTGCTGGTCCTGATGGTGGGGGGTGGTGATGTTCACCCTGGGGTTCGCCGGCTGC TGGAGCGAAAAGGGTGTGCTGTCCGACCTCACCAAAGTGACCCGGATGCATGGAATCGAC AGCTACAACATCATCTTCTGGTTGGCTGGAGTTGTCTTCCTTGGAGTCGGGCTGTGGGCA 186 ATGCACTATTATAGATACTCTAACGCCAAGGTCAGCTGCTGCTACAAGTACCTCCTTTTC ATGCACTATTATAGATACTCTAACGCCAAAGTCAGCTGCTGGTACAAGTACCTCCTTTTC 126 GTGGGGGCTCTGCGGGAGAATATCTGCTTGCTCAACTTTTTCTGTGGCACCATCGTGCTC CCTGTGGTGCTGGTCCTGATGGTGGGCGTGGTGATGTTCACCCTGGGGTTCGCCGGCTGC TEGAGCGAAAAGGGTGTGCTGTCCGACCTCACCAAAGTGACCCGGATGCATGGAATCGAC 246 AGCTACAACATCATCTTCTGGTTGGCTGGAGTTGTCTTCCTTGGAGTCGGGCTGTGGGTA 120 600 666 426 366 306 180 60 786 726 540 606 480 546 420 486 360 300 240

Query Match Best Local

Similarity

58.3**%**; 99.8**%**;

Score 809.8; DB 22 Pred. No. 2.7e-203;

Length

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RESULT 12
AAF90659
AAF90659
AC AAF90
AC AC AC AAF90
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                                                                                                   CC The invention relates to novel secreted/transmembrane proteins, and CC nucleic acids encoding them. The novel proteins are designated TANGO 339, CC TANGO 353, TANGO 356, TANGO 365, TANGO 369, TANGO 369, TANGO 383, TANGO CC 393, TANGO 340, MANGO 346 and MANGO 349 and are of human origin, and a CC invention also encompasses fragments and variants of the proteins of the invention. The CC invention, and nucleic acids encoding them. The invention additionally CC relates to host cells comprising a nucleic acid of the invention; methods CC for a protein of the invention; and methods of identifying approach of the invention; and methods for detecting a protein or CC nucleic acid of the invention; and methods for detecting a protein or CC bind to or modulate the activity of a protein of the invention. The novel CC secreted proteins, nucleic acids encoding them, and antibodies against them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression or activity of the secreted conductors of expression or activity, which may be useful in the treatment of disorders associated with the proteins of the invention of the invention e.g., cancers and immunological disorders. The present contains the proteins of the invention of the invention of the invention of the present contains of the invention of the invention of the present contains of the invention of the invention of the invention of the invention e.g., cancers and immunological disorders. The present contains of the invention of the inve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding secreted TANGO and MANGO polypeptides, useful for the prevention, diagnosis and treatment of, e.g. cancers and imm disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-138647/14.
P-PSDB; AAB87137.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 283; 332pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUL-1999;
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20,
                                                                           represents cDNA encoding human TANGO protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sharp JD,
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Sequence

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RESULT 13
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standard;

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SECX protein; human; secreted; membrane-associated; proliferation regulator; differentiation regulator;

cancer;

DNA.

non-malignant tumour;

Human tetraspanin-like protein splice variant SECX 3911675-2

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             ATCGAGGCAGTGAAGGCCGGCCATCACTTCTGA
                                                     GACTGGGACCTCAACGTCTACTTCAATTGCAGCGGTGCCAGCTACAGCCGAGAGAAGTGC
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                                                                                 ATCGCCATCTCGCTGTTGCAGATATTTGGCATCTTCCTGGCAAGGACGCTGATCTCAGAC
                                                                                                              GGATATGATGTCAGGATTCAGCTGAAGAGCAAGTGGGATGAGTCCATCTTCACGAAAAGGC
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                                                                                                                                                                                                                                                                                                                                                   predisposition to, a disease associated with altered levels of SECX proteins and nuclectides. The SECX proteins are also useful to screen compounds that modulate SECX activity or expression. The interaction of a SECX protein with other cellular proteins may be useful to modulate the activity of a partner protein, cellular proliferation, cellular cell survival. SECX nucleotides are useful for the recombinant expression of SECX protein, and may be used detect SECX mRNA or genetic lesions in the SECX gene. They may also be used to modulate SECX expression (e.g., using antisense oligonuclectides). SECX nucleic a biological sample, and in forensic biology. SECX primers or probes are useful for detecting the presence of SECX nucleotides) are cultures for contamination. Diseases that may be treated or prevented using SECX proteins or nucleotides and for screening tissue cultures for contamination. Diseases that may be treated or prevented using SECX proteins or nucleotides and for screening the presence of SECX nucleotides and for screening the presence of SECX nucleotides and for screening this protein and screening the presence of SECX nucleotides and for screening 
                                                                                                                                                                                                                                                                                                                                                                                                                               skin disorders, cardiovascular disorders, atherosclerosis, restenosis, neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical or traumatic wounds, spinal cord injury), and skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids which encode human SECX proteins (AAB23029-B23048). The SECX proteins of the invention are either secreted or membrane-associated proteins and act as regulator of cellular proliferation and differentiation. SI proteins or nucleotides are useful for diagnosing the presence of or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colorectal carcinoma, prostate cancer), benign tumours, immune disorders (including autoimmune diseases, transplant rejection, allergies, AIDS), (infections, inflammatory disorders, arthritis, haematopoietic disorders,
                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human membrane associated or secreted polypeptides and polynucleotides useful for diagnosis, prevention and treatment of pathological states such as cancer, immune, cardiovascular and neurological disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Fig 8B; 151pp; English.
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                                                                                        Human; chromosome mapping; gene mapping; gene therapy;
food supplement; medical imaging; diagnostic; genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC polypertide (II) sequences. (I) is useful as hybridisation probes, CC polyperase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical cimaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynuclectide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. As564197-As594564 represent novel human CC unit of the sequences of this patent did not appear in the printed constitution, but was obtained in electronic format directly from WIPO at figure in the printed products of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID No 16471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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вР;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 A; 168 C; 180 G; 146 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.5%;
98.8%;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 589.8;
Pred. No. 2.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.3e-145;
nes 7;
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RESULT 15
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Secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport and the blophylaxis of cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is the coding sequence for a human protein which has at least one hydrophobic domain. The protein encoded by the present sequence may be a secretory or a membrane protein. The encoded protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopolesis activity, tissue growth activity, haematopolesis activity, chemotactic/chemokinetic activity, haemostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-1998;
22-DEC-1998;
16-MAR-1999;
27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biophylaxis; signal receptor; ion channel; transporter; immunostimula immunosuppressant; haematopolesis regulator; chemotactic; chemokineti haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer;
                                                                                                                                                                                                                                                                                                                 Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                              Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200029448-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrophobic domain protein cDNA HP02956 isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                    activities e.g. immunomodulatory, antiinflammatory, hemostatic, thrombolytic -
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98JP-0364315.
99JP-0069811.
99JP-0119299.
99JP-0138169.
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differentiation induction; mater
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Best Local Similarity
Matches 638; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and thrombolytic activity, anti-inflammatory activity and tumour inhibition activity. The present sequence could therefore be used treatment of autoimmune disease, Alzheimer's disease, Parkinson's disease, and cancer via gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 639 BP; 131 A; 163 C; 188 G; 157 T; 0 other;
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                                                                             GGATATGATGTCAGGATTCAGCTGAAGAGCAAGTGGGATGAGTCCATCTTCACGAAAGGC
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                                       ATCGCCATCTCGCTGTTGCAGATATTTGGCATCTTCCTGGCAAGGACGCTGATCTCAGAC
                                                 ATCGCCATCTCGCTGTTGCAGATATTTGGCATCTTCCTGGCAAGGACGCTGATCTCAGAC
                                                                                                                     GGATATGATGTCAGGATTCAGCTGAAGAGCAAGTGGGATGAGTCCATCTTCACGAAAGGC
                                                                                                                                                            GGGGTCCCCTTCTCCTGCGTGCCAGATCCTGCGCAAAAAGTTGTGAACACACAGTGT
                                                                                                                                                                                                                                          -----TAACCAGTGCTGTGGCGCATATGGCCCTGAA
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ATCGAGGCAGTGAAGGCCGGCCATCACTTC
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milarity 78.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 456.4;
Pred. No. 3.3e
0; Mismatches
 639
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Search completed: December 19, Job time : 268 secs

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Minimum DB :
Maximum DB :
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-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MARRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN-0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM-ext -HEARSIZE=500 -MILIEN=0 -MAXLEN=200000000
-USER-US09905674_@CGN_1_1_125_@runat_16122002_111845_6745 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -KGAPOP=10 -KGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result

Query

No.	Score	Match	Length	DB	ID	Description
υL	1449	100.0	മ	22	AAF90629	TANGO
ω ,	1449		2715	22	AAF90628	
4	1446		œ	22	AAF90656	TANGO 339
51	1446		813	22	AAF90657	TANGO 339
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10	1419		1428	21	AAA93623	an tetraspanin
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	1120.5		639	21	AAA60182	don
	1120.5		2367	21	AAA60192	Hydrophobic domain
14	1049	72.4	816	21	AAA93675	Human tetraspanin-
15	936		601	23	AAS80667	DNA encoding novel
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21	841.5		2538	24	AAD21883	Human TM4SF recept
22	829		1174	22	AAC90015	невел16
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26	729.5		1110	24	ABA90960	Human polynucleoti
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35	550		2638	24	ABL90058	Human polynucleotí
36	541		1187	23	ABL07929	
37	522.5	36.1	.3244	23	ABL07928	
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ALIGNMENTS

RESULT 1 AAF90629

AAF90629 standard; cDNA; 813 ВP

04-MAY-2001 (first entry)

Human TANGO 339 cDNA ORF, SEQ ID NO:2

Secreted protein; transmembrane protein; TANGO; human; drug screening; activity modulator; expression modulator; cancer; immunological disorder; cytostatic; immunomodulatory; gene therapy; ss.

Homo sapiens.

WO200109162-A2. B

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                                                                                                                                                                                                                                                                                                                                                                                                                                         CC The invention relates to novel secreted/transmembrane proteins, and CC nucleic acids encoding them. The novel proteins are designated TANGO 339, CC TANGO 353, TANGO 356, TANGO 368, TANGO 369, TANGO 383, TANGO CC 393, TANGO 402, MANGO 346 and MANGO 349 and are of human origin, and a CC murine TANGO 393 is also included within the scope of the invention. The CC invention also encompasses fragments and variants of the proteins of the cinvention, and nucleic acids encoding them. The invention additionally CC relates to host cells comprising a nucleic acid of the invention; methods for the protein of the invention; and antibody specific CC for a protein of the invention; methods for detecting a protein or concleic acid of the invention; and methods of identifying agents which CC bind to or modulate the activity of a protein of the invention. The novel cassociated with inappropriate expression or activity of the secreted proteins. The prevention, diagnosis and treatment of diseases cassociated with inappropriate expression or activity, which may be used to concention e.g., cancers and immunological disorders. The present CC invention e.g., cancers and immunological disorders. The present concention of the invention of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding secreted TANGO and MANGO polypeptides, useful for the prevention, diagnosis and treatment of, e.g. cancers and immune
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DB; AAB87034, AAB87035, AAB87036
 GTGGGGGCTCTGCGGGAGAATATCTGCTTGCTCAACTTTTTCTGTGGCACCATCGTGCTC
              ValGlyAlaLeuArgGluAsnIleCysLeuLeuAsnPhePheCysGlyThrIleValLeu
                                                                    ProValValLeuValLeuMetValGlyValValMetPheThrLeuGlyPheAlaGlyCys
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                                                                                                                                                                                                        protein, TSPAN-7 encoding cDNA
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                                                                                                                                                                                  protein; TSPAN-7; hyperproliferative disorder;
se; prostate cancer; antisense therapy; tumour;
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                                                                                                                                  "Human TSPAN-7
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Reinhard CJ, Garcia

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New inhibitor of tetraspan protein useful for reducing the exportantivities of tetraspan protein in cells, and for treating hyperproliferative disorder, especially cancer in a mammal -
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The invention relates to novel secreted/transmembrane proteins, and Cnucleic acids encoding them. The novel proteins are designated TANGO 339, CC TANGO 353, TANGO 358, TANGO 368, TANGO 368, TANGO 369, TANGO 383, TANGO 37 TANGO 37 TANGO 369, TANGO 389, TANGO 37 TANGO 37 TANGO 37 TANGO 37 TANGO 37 TANGO 37 TANGO 389, TANGO ANGO TANGO TANGO TANGO TANGO TANGO TANGO TANGO TANGO TANGO TAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 219-220; 332pp; English.
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P-PSDB; AAB87034, AAB87035, AAB87036.
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                                                                                                                                                              CC The invention relates to novel secreted/transmembrane proteins, and concleic acids encoding them. The novel proteins are designated TANGO 339, TANGO 353, TANGO 358, TANGO 365, TANGO 368, TANGO 369, TANGO 383, TANGO 393 is also included within the scope of the invention. The convention also encompasses fragments and variants of the proteins of the invention, and nucleic acids encoding them. The invention additionally crelates to host cells comprising a nucleic acid of the invention; methods for the production of a protein of the invention; an antibody specific for a protein of the invention; methods for detecting a protein or nucleic acid of the invention; methods of bind to or modulate the activity of a protein of the invention. The novel creatment by used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression or activity of the secreted proteins. The secreted proteins of the invention may also be used to identify modulators of expression or activity, which may be used to the treatment of disorders associated with the proteins of the invention of the invention e.g., cancers and immunological disorders. The present convention and immunological disorders. The present
                                                                                                                                         US-09-905-674-2
                                                                                    Score:
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The invention relates to novel secreted/transmembrane proteins, and concleic acids encoding them. The novel proteins are designated TANGO 339, CANGO 353, TANGO 358, TANGO 356, TANGO 368, TANGO 369, TANGO 383, TANGO 393, TANGO 346 and MANGO 349 and are of human origin, and a convention also encompasses fragments and variants of the invention. The invention, and nucleic acids encoding them. The invention additionally convention of the invention of a protein of the invention; an antibody specific for the production of a protein of the invention; an antibody specific concleic acid of the invention; and methods for detecting a protein or nucleic acid of the invention; and methods of identifying agents which indicated acid of the invention; and methods of identifying agents which concleic acid of the invention; and methods of identifying agents which concleic acid of the invention; and methods of identifying agents which concleic acid of the invention; and antibodies against the secreted proteins, nucleic acids encoding them, and antibodies against the proteins. The secreted proteins of the invention may also be used to concleit the may be used to the treatment of disorders associated with the proteins of the invention may be used to the treatment of disorders associated with the proteins of the invention.

CC invention e.g., cancers and immunological disorders. The present convention are represents cDNA encoding human TANGO protein of the invention.
Nucleic acids encoding secreted TANGO and MANGO polypeptides, useful for the prevention, diagnosis and treatment of, e.g. cancers and immune disorders - \,
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    and MANGO 349
                                                                                                           English.
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    are of human
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                    NGO 339,
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cc murine TANGO 393 is also included within the scope of the invention. The cinvention also encompasses fragments and variants of the proteins of the clivention, and nucleic acids encoding them. The invention additionally cc relates to host cells comprising a nucleic acid of the invention; methods cf or the production of a protein of the invention; an antibody specific cc for a protein of the invention; and methods for detecting a protein or culcic acid of the invention; and methods of identifying agents which cs secreted proteins, nucleic acids encoding them, and antibodies against them may be used in the prevention, diagnosis and treatment of diseases cc associated with inappropriate expression or activity of the secreted cc identify modulators of expression or activity, which may be useful in cc identify modulators of expression or activity, which may be useful in cc invention e.g., cancers and immunological disorders. The present cc sequence represents cDNA encoding human TANGO protein of the invention.

Sequence 813 B₽; 163 Α, 212 Ç 235 <u>.</u> 203 Ŧ; 0 other;

Alignment Pred. No.:

Scores:

No.:

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DB:
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                                                                            GlyValProPheSerCysCysValProAspProAlaGlnLysValValAsnThrGlnCys
                                                  ValGlyAlaLeuArgGluAsnIleCysLeuLeuAsnPhePheCysGlyThrIleValLeu
                                                                                                                                                                                         ProValValLeuValLeuMetValGlyValValMetPheThrLeuGlyPheAlaGlyCys
                                                                                                                                                                                  CCTGTGGTGCTGGTCGTGGTGGGCGTGGTGATGTTCACCCTGGGGTTCGCCGGCTGC
                                                                                                                                ATCTTCTTCCTGGAGCTGGCTGTGGCCGTGCTGGCCTTCCTGTTCCAGGACTGGGTGAGG
                                                                                                                                      IlePhePheLeuGluLeuAlaValAlaValLeuAlaPheLeuPheGlnAspTrpValArg
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1445.00
99.63%
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Conservative:
Mismatches:
Indels:
Gaps:
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RESULT 7
AAF90659
ID AAF99
XX AAF99
XX AAF99
XX Secy
XX Secy
KW Secy
KW Cytc
XX HOMC
PD 08-F
XX AI-J
XX HOMC
PT Fras
PF 31-J
XX HOM
XX
                                 The invention relates to novel secreted/transmembrane proteins, and convocation and convocations are designated TANGO 339, TANGO 358, TANGO 358, TANGO 368, TANGO 369, TANGO 383, TANGO 393, TANGO 358, TANGO 369, TANGO 369, TANGO 383, TANGO 383, TANGO 393, TANGO 393 is also included within the scope of the invention. The convention and nucleic acids encoding them. The invention additionally relates to host cells comprising a nucleic acid of the invention, methods for the production of a protein of the invention; an antibody specific for a protein of the invention; methods for detecting a protein or concluded a protein of the invention; and methods of identifying apents which bind to or modulate the activity of a protein of the invention. The novel concreted proteins, nucleic acids encoding them, and antibodies against them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression or activity of the secreted proteins. The secreted proteins of the invention may also be used to the treatment of disorders associated with the proteins of the invention of the invention e.g., cancers and immunological disorders. The present of the invention of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding secreted TANGO and MANGO polypeptides, useful for the prevention, diagnosis and treatment of, e.g. cancers and imm disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-138647/14.
P-PSDB; AAB87137.
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Sequence 813 BP; 163 A; 212 C;

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202 T;

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23-MAR-2000 AAZ65259;

(first entry)

standard;

DNA;

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AC AAZ6
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                                                                                                                                                                                              GlyTyrAspValArgIleGlnLeuLysSerLysTrpAspGluSerIlePheThrLysGly
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Alignment Scores:
                                                                                                    AA265250 to AA265350 represent 97 isolated human secreted protein genes. This sequence was found to be present on human chromosome 10.

AAY76124 to AAY76223 represent the secreted proteins encoded by the 97 human genes. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions.

C. e. g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 97 genes, based on which tissues they care most highly expressed in, and include developing products for the CC diagnosis or treatment of cancer, tumours, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, cautoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin clasorders, atherosclerosis, diabetes, cardiovascular disorders, kidney consorters, digestive/endocrine disorders, infections and AIDS. The collypeptides are also useful for identifying their binding partners.

The sequences shown in AAY76224 to AAY76424 represent fragments of the
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18-MAY-1998;
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18-MAY-1998;
18-MAY-1998;
18-MAY-1998;
18-MAY-1998;
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18-MAY-1998;
18-MAY-1998;
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Olsen
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                                                                                                                                                                                                                                                                                                                                                                                                      Page 301-302;
                                                                                                                                                                                                                                                                                                                                                                                                                                ed human genes and the secreted polypeptides they encode, diagnosis and treatment of e.g. cancers, neurological immune diseases, inflammation or blood disorders -
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Shi Y, Young
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      human diagnostic
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      protein #27820
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CC Note: The sequence data for this patent did not appear in the printed content pulps and not forential content pulps and not septimine and not appear in the printed content pulps and not produce of the number of the pulps and the printed content pulps and produce of the number of the pulps and produce of the numbe
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                            SerTyrAsnIleIlePheTrpLeuAlaGlyValValPheLeuGlyValGlyLeuTrpAla
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DB; ABG27829.
TGGAGCGAAAAGGGTGTGCTGTCCGACCTCACCAAAGTGACCCGGATGCATGGAATCGAC
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imaging; diagnostic; genetic disorder; ss
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09-MAR-2000; 2000WO-US06280

14-SEP-2000

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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human membrane associated or secreted polypeptides and polynucleotides useful for diagnosis, prevention and treatment pathological states such as cancer, immune, cardiovascular and neurological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAR-1999; 99US-0123667
08-MAR-2000; 2000US-0123667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the invention are either secreted or membrane associated proteins and act as regulator of cellular proliferation and differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids which encode human SECX proteins (AAB23029-B23048). The SECX proteins
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                                                                                                                                                                                                                                                                                                                                                       autoimmune disease; allergy; Alzheimer's disease; cognitive disorder schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AIDS; leukaemia; therapy; chromosome 10; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC AA265250 to AA265350 represent 97 isolated human secreted protein genes. CC This sequence was found to be present on human chromosome 10. AAY76124 to AAY76223 represent the secreted proteins encoded by the 97 cc AAY76124 to AAY76223 represent the secreted proteins encoded by the 97 cc e.g. by protein or gene therapy. Also pathological conditions, cc e.g. by protein or gene therapy. Also pathological conditions can be cidagnosed by determining the amount of the new polypeptides in a sample cc or by determining the presence of mutations in the new genes. Specific cc uses are described for each of the 97 genes, based on which tissues they cc are most highly expressed in, and include developing products for the cc diagnosis or treatment of cancer, tumours, developmental abnormalities cand foetal deficiencies, blood disorders, diseases of the immune system, cc disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skiney cc disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney cc disorders, diseastey inflammation, allergies, Alzheimer's and AIDS. The corrected mortaine in AAY76224 to AAY76424 represent fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAY-1998;
18-MAY-1998;
18-MAY-1998;
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Olsen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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[[[]]]
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                                                                                                               TGGAGCGAAAAGGGTGTGCTGTCCGACCTCACCAAAGTGACCCGGATGCATGGAATCGAC
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Brewer LA, Soppet DR;
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22-DEC-1998;
16-MAR-1999;
27-APR-1999;
19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; membrane protein; hydrophobic domain; proliferation control; differentiation induction; material transport; blophylaxis; signal receptor; ion channel; transporter; immunosuppressant; haematopoissis regulator; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
                                                                                                                                                                                                                                                                                                          25-MAY-2000
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98JP-0364315.
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99JP-0119299.
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P-PSDB;
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              AspTrpAspLeuAsnValTyrPheAsnCysSerGlyAlaSerTyrSerArgGluLysCys
                                                                     GlnAsnLeuIleAspSerLeuGlnLysAlaAsnGlnCysCysGlyAlaTyrGlyProGlu
                                                                                                                                              Asp \texttt{ArgPheArgGluPhePheGluSerAsnIleLysSerTyrArgAspAspIleAspLeum}
                                                                                                                                                                                                                                        GTGGGGGCTCTGCGGGAGAATATCTGCTTGCTCAACTTT
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DB; AAB12120.
GACTGGGACCTCAACGTCTACTTCAATTGCAGCGGTGCCAGCTACAGCCGAGAGAAGTGC
                                                                                                                                                                                                          IlePhePheLeuGluLeuAlaValAlaValLeuAlaPheLeuPheGlnAspTrpValArg
                                                                                                                                                                                                                                                                     ValGlyAlaLeuArgGluAsnIleCysLeuLeuAsnPhePheCysGlyThrIleValLeu 100
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                                                                                                                                                                                                                                                                                                   CCTGTGGTGCTGGTCCTGATGGTGGGCGTGGTGATGTTCACCCTGGGGTTCGCCGGCTGC
                                                                                                                                                                                                                                                                                                                                ProValValLeuValLeuMetValGlyValValMetPheThrLeuGlyPheAlaGlyCys
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22-DEC-1998;
16-MAR-1999;
27-APR-1999;
19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; membrane protein; hydrophobic domain; proliferation control; differentiation induction; material transport; biophylaxis; signal receptor; ion channel; transporter; immunostimulant; immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer;
                                                             Claim
                                                                                   activities e.g. immunomodulatory, antiinflammatory, chemokinetic, hemostatic, thrombolytic
                                                                                                    proteins, useful in research and diagnostics and having various
                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                    17-NOV-1999;
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)B; AAB12120.
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98JP-0364315.
99JP-0069811.
99JP-0119299.
99JP-0138169.
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secretory proteins play important roles in the proliferation control, differentiation induction, the material transport and the biophylaxis cells, Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is the coding sequence for a human protein which has at least one hydrophobic domain. The

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein encoded by the present sequence may be a secretory or a membrane protein. The encoded protein may have cytokine and cell proliferation/differentiation activity; immune stimulating or suppressing activity, haematopoiesis activity, tissue growth activity, haematopoiesis activity, tissue growth activity, haemostatic activin/inhibin activity, ohemotactic/chemokinetic activity, haemostatic and thrombolytic activity, anti-inflammatory activity and tumour inhibition activity. The present sequence could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2367 BP;
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CysIleGlnAlaLeuGluSerTrpLeuProArgAsnIleTyrIleValAlaGlyValPhe
                                                                                                                                                  GlyTyrAspValArgIleGlnLeuLysSerLysTrpAspGluSerIlePheThrLysGly
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                                                                                                                                   GGATATGATGTCAGGATTCAGCTGAAGAGCAAGTGGGATGAGTCCATCTTCACGAAAGGC
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                                                                 GTGGGGGCTCTGCGGGAGAATATCTGCTTGCTCAACTTT------
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prevented using SECX proteins or nucleotides include cancer (e.g., colorectal carcinoma, prostate cancer), benign tumours, immune disorders

colorectal carcinoma, prostate cancer), benign tumours, immune disorder (including autoimmune diseases, transplant rejection, allergies, AIDS),

disorders,

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CC of the invention are either secreted or membrane-associated proteins
CC and act as regulator of cellular proliferation and differentiation. SECX
CC proteins or nucleotides are useful for diagnosing the presence of, or
CC predisposition to, a disease associated with altered levels of SECX
CC proteins and nucleotides. The SECX proteins are also useful to screen
CC compounds that modulate SECX activity or expression. The interaction of
CC compounds that modulate SECX activity or expression. The interaction of
CC a SECX protein with other cellular proteins may be useful to modulate
CC the activity of a partner protein, cellular proliferation, cellular
CC differentiation and cell survival. SECX nucleotides are useful for the
CC recombinant expression of SECX protein, and may be used detect SECX mRNA
CC or genetic lesions in the SECX gene. They may also be used to modulate
CC SECX expression (e.g., using antisense oligonucleotides). SECX nucleic
CC acid sequences are also useful for identifying a cell or tissue type in
CC acid sequences are also useful for identifying a cell or tissue type in
CC useful for detecting the presence of SECX nucleotides and for screening
CC tissue cultures for contamination. Diseases that may be treated or
Creamented mains serve proteins or nucleotides and concer (e.g.
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                                                                                                                                                                                                                                                                                                                                                                                             Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids which encode human SECX proteins (AAB23029-B23048). The SECX proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathological states such as cancer, immune,
neurological disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human membrane associated or secreted polypeptides and polypucleotides useful for diagnosis, prevention and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAR-1999;
08-MAR-2000;
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Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic
                                  DNA encoding novel human diagnostic protein #16471.
                                                          13-FEB-2002
                                                                                                       AAS80667
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                     cc polypeptide (II) sequences. (I) is useful as hybridisation probes, cc polymerase chain reaction (PCR) primers, oligomers, and for chromosome cc and gene mapping, and in recombinant production of (II). The cc polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques cc to restore normal activity of (II) or to treat disease states involving cc (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating cc disgrders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cc diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cannot acid sequences. AAS64197-AAS94564 represent novel human cc anticological active with the sequence of the invention.

CC Note: The sequence data for this patent did not appear in the printed can the print of the products of the printed of the sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of muta responsible for genetic disorders or other traits and to ass biodiversity -
                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes.
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23-AUG-2000;
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Search completed: December 19, 2002, 06:26:57 Job time: 269 secs

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Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q-/cgn2_1/USPTO_spool/US09905674/runat_16122002_111847_6882/app_guery.fasta_1.455
-DB-Published_Applications_NA -QFMT-fastap -SUFFIX-rnpb -MINMATCH=0.1
-LOOPEL-0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALION=200 -THR SCORE-pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT-pto -NOM-ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER-US09905674_@CGN_1_1_21_@runat_16122002_111847_6882
-NCPG-6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEDUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                                                                                                                                                                '/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
'/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
'/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
'/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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-09-981-876-8	S-09-115-45	S-09-822-827-	09-030-606-	S-09-780-669-1	S-09-759-143	S-10-012-896-11	09-232-880-11	-09-998-598-	799-777-79	-09-822-830A-4	-09-969-708-13	-09-925-301-193	-09-880-107-234	9-833-263-	s-09-922-217-105	10-025-380-1052	s-09-922-217-	-10-025-380-1	-09-922-217-11	-10-025-380-1120	09-822-830A-5	-09-795-380-19	-09-925-301-539	S-09-880-107-2	S-09-967-768A-32	S-09-925-302-31	S-09-822-849A-5	-09-954-531-134	-09-822-830A-	-09-925-301-39	09-823-35	-09-729-674-8	S-10-042-417-37	5-09-895-828-430	S-09-783-590-10	S-09-823-356-31	64-864-27	S-10-052-586-2	-09-875-440-1	US-09-729-674-169	
Sequence 82, Appl	111,	111,	equenc	e 111.	Sequence 111,		equence 111,	equence 563,	e 79	equence 421	132	193	2242	1052	Sequence 1052	1052	Sequence 1119,	e 1119,	e 1120,	e 1120,	equence 597,	19,	equence 539,	equence 2351	equence 323.	e 31.	Sequence 51,	quence 1349,	equence 64	392	equence 32,	89.	equence 37, A	equence 430, Ap	equence 10353.	equence 31, App	e 279, Ap	Sequence 277,	quence 1, Appli	Sequence 169, App	

## ALIGNMENTS

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RESULT 1

US-09-925-299-205
; Sequence 205, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 50/124,270
PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 205
LENGTH: 1655
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1548)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (1559)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
; NAME/KEY: misc_feature
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NAME/KEY: misc_feature
; LOCATION: (1623)
; OTHER INFORMATION: n equals a
; NAME/KEY: misc_feature
; LOCATION: (1643)
; OTHER INFORMATION: n equals a
US-09-925-299-205
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                                                                CysCysValProAspProAlaGlnLysValValAsnThrGlnCysGlyTyrAspValArg
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                       CTGCAGATATTTGGGATATGCCTGGCCCAGAATTTGGTTAGCGATATCGAAGCTGTCAGG
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Sequence 3, Application US/09934268; Patent No. US20020172986A1; GENERAL INFORMATION:
APPLICANT: Leiby, Kevin R.
APPLICANT: Leiby, Kevin R.
TITLE OF INVENTION: 23228, A NOVEL HUMAN TETRASPANIN FAM.
TITLE OF INVENTION: MEMBER AND USES THEREOF
FILE REFERENCE: 10448-079001
CURRENT APPLICATION NUMBER: US/09/934,268; CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 60/226,612
PRIOR APPLICATION NUMBER: 60/226,612
PRIOR APPLICATION NUMBER: 60/226,612
PRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 813
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CCCTTCTCCTGCTGCGTCAGGGACCCTGCGGAGGATGTCCTCAACACCCCAGTGTGGCTAC
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US-09-934-268-1
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Patent No. US20020172986A1
GEMERAL INFORMATION:
APPLICANT: Leiby, Kevin R.
TITLE OF INVENTION: 23228, A NOVEL HUMAN TETRASPANIN FAMILY
TITLE OF INVENTION: MEMBER AND USES THEREOF
FILE REFERENCE: 10448-079001
CURRENT APPLICATION NUMBER: US/09/934,268
CURRENT APPLICATION NUMBER: 60/226,612
PRIOR APPLICATION NUMBER: 60/226,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-08-21
NUMBER OF SEC ID NOS: 4
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
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NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2538
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APPLICANT: Shi et a
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                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/US01/11130
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,336
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/972,970 CURRENT FILING DATE: 2001-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Shi et al. TITLE OF INVENTION: TM4SF Receptor Polynucleotides, Polypeptides, and Antibodies FILE REFERENCE: PT056p1
                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo
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                                  APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Liss
APPLICANT: Collins-Racie, Liss
APPLICANT: Evans, Cheryl
APPLICANT: Evans, Cheryl
APPLICANT: Herbary, Maurice
APPLICANT: Agostino, Michael J
APPLICANT: Steininger II, Robe
APPLICANT: Spaulding, Vikki
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Genetics Institute,
TITLE OF INVENTION: SECRETED PR
FILE REFERENCE: 6055-64X
                                                                                                                                                                                                                                                    Sequence 169, Application US/09729674 Patent No. US20010039335A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           -09-729-674-169
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
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Treacy, Maurice
Agostino, Michael J.
Steininger II, Robert
Spaulding, Vikki
Wong, Gordon G.
Clark, Hilary
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LaVallie, Edward R.
Collins-Racie, Lisa
Evans, Cheryl
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Genetics Institute,
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; ORGANISM: Homo
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SEQ ID NO 169
LENGTH: 1110
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US-09-875-440-1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: NEOPLASTIC DISEASE USING NET-4 MODULATORS
FILE REFERENCE: pp-01701, 002/200130, 522
CURRENT APPLICATION NUMBER: US/09/875,440
CURRENT FILING DATE: 2001-06-05
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OTHER INFORMATION: assay
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ORGANISM: Homo
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 ValTyrPheAsnCysSer 171
                                                                                             PhePheGluSerAsnIleLysSerTyrArgAspAspIleAspLeuGlnAsnLeuIleAsp 145
                                                                                                                                                                                          GAAAACACTTTCCTTCTCAAGTTTTTTTCTGTGTTCCTGGGAATTATTTTCTTCCTGGAG
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                            TTCACCCAGGAATATTGGCAGTGCTGTGGGGCTTTTGGAGCTGATTGGAACCTAAAT
                                       SerLeuGlnLysAlaAsnGlnCysCysGlyAlaTyrGlyProGluAspTrpAspLeuAsn 165
                                                                                                                                     CTCACTGCCGGAGTTCTAGCATTTGTTTTCAAAGACTGGATCAAAGACCAGCTGTATTTC
                                                                                                                                                              LeuAlaValAlaValLeuAlaPheLeuPheGlnAspTrpValArgAspArgPheArgGlu
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RESULT 7
US-10-052-586-277
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PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR APPLICATION NUMBER: 60/063121
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PRIOR FILING DATE: 1997-10-24
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CURRENT FILING DATE: 2002-01-15
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OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063486
OR FILING DATE: 1997-10-21
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OR FILING DATE: 1997-10-31
OR APPLICATION NUMBER: 60/065311
OR FILING DATE: 1997-11-13
OR APPLICATION NUMBER: 60/066120
OR FILING DATE: 1997-11-21
OR APPLICATION NUMBER: 60/066466
APPLICATION NUMBER: 60/0
FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/0
FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/068017
FILING DATE: 1997-12-18
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OR APPLICATION NUMBER: 60/079786
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OR APPLICATION NUMBER: 60/080107
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OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/080327
OR APPLICATION NUMBER: 60/08033
OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/08104
OR FILING DATE: 1998-04-08
OR APPLICATION NUMBER: 60/081195
OR FILING DATE: 1998-04-09
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OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/083495
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Matches:
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FILING DATE: APPLICATION |

NUMBER: 60/087759: 1998-06-02

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OR APPLICATION NUMBER: 60/084414
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OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084640
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/085573
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OR APPLICATION NUMBER: 60/086392
OR FILING DATE: 1998-05-22
OR APPLICATION NUMBER: 60/086486
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OR APPLICATION NUMBER: 60/086486
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OR APPLICATION NUMBER: 60/087098
OR APPLICATION NUMBER: 60/087099
OR APPLICATION NUMBER: 60/087099
OR FILING DATE: 1998-05-28
OR APPLICATION NUMBER: 60/087099

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                             CURRENT APPLICATION UNDER: US/09/864,864
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 341
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 279
LENGTH: 873
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                       APPLICANT: Mannion, Jane
APPLICANT: Benson, Darin R.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.523
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xu, Jiangchun
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                               Secrist, Heather
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Query Match:
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                                                   Sequence 31, Application Upatent No. US20010025098A1 GENERAL INFORMATION:
           APPLICANT: Tang,
APPLICANT: Bands
APPLICANT: Lal,
 APPLICANT:
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Hillman, Jennifer L.
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; LOCATION: 959
; OTHER INFORMATION: a,
US-09-823-356-31
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LENGTH: 1175
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/039,307
PRIOR FILING DATE: 1998 March 13
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PERL Program
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TITLE OF INVENTION: HUMAN MEMBRANE SPANNING
FILE REFERENCE: PF-0489-1 CON
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ORGANISM: Homo sapiens
FEATURE:
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OTHER INFORMATION: Inc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               386 AGCTTTTTCATCGTCCTGTTGGTCATCCTCCTAGCAGAGCTGATCTTACTCATCCTCTTC
                                                          171 SerGlyAlaSerTyrSerArgGluLysCysGlyValProPheSerCysCysValProAsp 190
                                                                                                                                                                                      133 SerTyr-----ArgAspAspIleAspLeuGlnAsnLeuIleAspSerLeuGlnLysAla
                                                                                                                                                                                                                                                  113 PheLeuPheGlnAspTrpValArgAspArgPheArgGluPhePheGluSerAsnIleLys 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 CTGCTGGGAGTGGGCATCTGGCTCTCCGTGTCCCAAGGCAACTTTGCC-----ACCTTC
                                                                                                                                                                                                                                                                                                                                                                                                         266 TCCCCCAGCTTCCCTTCGTTGTTTGCAGCCAACCTGGTCATTGCCATAGGCACCATTGTC
                                                                                                                                                                                                                                                                                                             93 PhePheCysGlyThrIleValLeuIlePhePheLeuGluLeuAlaValAlaValLeuAla
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ProAlaGlnLysValValAsnThrGln---CysGlyTyrAspValArgIleGlnLeuLys 209
                                 CTGGGGGAGAAC-----
                                                                                            ATGCGATGCTGTGTGTCACTGACTACACAGACTGG
                                                                                                                                                         CTGTACCACACCGAGAACAACGTGGGGGCTGAAGAACGCCTGGAACATCATCCAGGCTGAG
                                                                                                                                                                                                                      ATGGTGACGGGCTTCCTCGGCTGCCTGGGGGGCCATCAAGGAAAACAAGTGCCTCCTCCTC
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Guegler, Karl J.
Kaser, Matthew R.
Baughn, Mariah R.
Shah, Purvi
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US-09-783-590-10353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/783,590 CURRENT FILING DATE: 2000-02-15
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APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences,
FILE REFERENCE: PO-16.2C1
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                 LOCATION: (361)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
LOCATION: (394)
                                                                                LOCATION: (340)
OTHER INFORMATION: n e
NAME/KEY: misc feature
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LOCATION: (331)
OTHER INFORMATION: n equals
                                                                                                                               OTHER INFORMATION: n equals NAME/KEY: misc feature
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OTHER INFORMATION: n equals
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INFORMATION: n equals a,t,g,
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LOCATION: (408)

OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (411)

OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (415)

OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (415)

OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (436)

OTHER INFORMATION: n equals a,t,g, or OTHER I
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APPLICANT: Wang, Tongtong

APPLICANT: McNeill, Patricia D.

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Henderson, Robert A.

APPLICANT: Henderson, Robert A.

APPLICANT: Henderson, Robert A.

APPLICANT: Henderson, Robert A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.539

CURRENT APPLICATION NUMBER: US/09/895,828

CURRENT APPLICATION NUMBER: US/09/895,828

CURRENT FILING DATE: 2001-06-28

NUMBER OF 580 ID NOS: 473

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 430

LENGTH: 690

TYPE: DNA

ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
                                                                                                ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 11, 662
; OTHER INFORMATION: n = A,T,C or
US-09-895-828-430
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US-09-895-828-430
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Alignment Scores: Pred. No.:
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LOCATION: (400)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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RESULT 12 US-10-042-417-37 ; Sequence 37, Application US/10042417 ; Sequence 37, Application US/10042417 ; Patent NO. US20020123082A1 ; GENERAL INFORMATION: APPLICANT: Pagano, M. APPLICANT: Pagano, M. TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS FILE REFERENCE: 5914-090-999 ; CURRENT APPLICATION NUMBER: US/10/042,417 ; CURRENT FILING DATE: 2002-01-07 ; PRIOR APPLICATION NUMBER: 60/260,179 PRIOR APPLICATION NUMBER: 60/260,179 PRIOR FILING DATE: 2001-01-5 ; NUMBER OF SEQ ID NOS: 89 ; SOFFWARE: Patentin Ver. 2.0 ; SEQ ID NO 37 ; LENGTH: 368 ; TYPE: DNA ; ORGANISM: Homo sapiens ; FRATURE: ; NAME/KEY: modified_base	QY 263 Ala 263 ::: Db 585 AGT 587	Qy 243 IleSerLeuLeuGlnIlePheGlyIlePheLeuAlaArgThrLeuIleSerAspIleGlu	Qy 223 GlnAlaLeuGluSerTrpLeuProArgAsnIleTyrIleValAlaGlyValPheIleAla :::          ::     ::	Qy 203 AspValArgIleGlnLeuLysSerLysTrpAspGluSerIlePheThrLysGlyCysIle ::: ::::::::::::::::::::::::::::::::	Qy 183 ProPheSerCysCysValProAspProAlaGlnLysValValAsnThrGlnCysGlyTyr	Qy 163 AspLeuAsnValTyrPheAsnCysSerGlyAlaSerTyrSerArgGluLysCysGlyVal	Qy 143 LeuIleAspSerLeuGlnLysAlaAsnGlnCysCysGlyAlaTyrGlyProGluAspTrp ::::::    ::    ::     ::	Qy 123 PheArgGluPhePheGluSerAsnIleLysSerTyrArgAspAspIleAspLeuGlnAsn	Qy 103 PheLeuGluLeuAlaValAlaValLeuAlaPheLeuPheGlnAspTrpValArgAspArg :::   :::	Qy 83 AlaLeuArgGluAsnIleCysLeuLeuAsnPhePheCysGlyThrIleValLeuIlePhe	Qy 63 ValLeuValLeuMetValGlyValValMetPheThrLeuGlyPheAlaGlyCysValGly    ::::::::          :::    :::	US-09-905-674-2 (1-270) x US-09-895-828-430 (1-690)	Score: 282.00 Matches: 58 Percent Similarity: 50.25% Conservative: 43 Best Local Similarity: 28.86% Mismatches: 78 Query Match: 19.46% Indels: 22 DB: Gaps: 3
REATMENT OF		262	242 524	222	202 425	182 383	162 350	142 290	122 230	102	82 110		

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US-09-729-674-89; Sequence 89, Application US/09729674; Patent No. US20010039335A1
    Alignment Scores: Pred. No.:
                                                 ; ORGANISM: HOMO US-09-729-674-89
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Query Match:
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SEQ ID NO 89
LENGTH: 1797
TYPE: DNA
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
                                                                                                                                                                                                                         APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND
FILE REFERENCE: 6055-64X
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                                                                                                                                             NUMBER OF SEQ ID NOS: 283
                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/539,330 PRIOR FILING DATE: 2000-03-30
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Steininger II, Rok
Spaulding, Vikki
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LaVallie, Edward
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Treacy, Maurice
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                                            GENERAL INFORMATION:
APPLICANT: Tang, Y. To
APPLICANT: Bandman, o
APPLICANT: Lal, Preet
APPLICANT: Hillman, o
APPLICANT: Yue, Henry
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                                                                                                                                        Sequence 32, Application UPatent No. US20010025098A1
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Yue, Henry
Corley, Neil C.
Guegler, Karl J.
Kaser, Matthew R.
                                                              Hillman, Jennifer
                                                                             Lal, Preeti
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; OTHER INFORMATION: Incyte
US-09-823-356-32
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SOFTWARE: PERL Program
SEQ ID NO 32
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/039,307
PRIOR FILING DATE: 1998 March 13
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ORGANISM: Homo sapiens
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                         ValArgIleGlnLeuLysSerLysTrpAspGluSerIlePheThrLysGlyCysIleGln 223
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1694
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GCCACCTTCAAGGAGCGTCGGAACCTGCTGCGCGCCTGTACTTCATCCTGCTCCTCATCATC
                            GlyAlaLeuArgGluAsnIleCysLeuLeuAsnPhePheCysGlyThrIleValLeuIle 101
                                                                                                                                                        GluLysGly---ValLeuSerAspLeuThrLysValThrArgMetHisGlyIleAspPro
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                                                                                                TTTGGCATGATCTTCACGTGCTGCCTG-----TACAGGAGTCTCAAGCTGGAGCAC 844
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